

Db	1621	AGTTGTGGCAATACCTCTGTAATGAGTTGAGTGAAATGTCACCTGGATTTTTTTTATATATATACC	1680
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Db	1681	ACATGATGATACACATCTAAATATATAAACAAATCATAGTGTATGCATATGCAATTTGGCTAA	1740
Qy	1741	GAAGTATTAGTGATATACACTAGTGTCTATATATATAGTTTAAACCCCAACTTGGCAATGAA	1800
Db	1741	GAAGTATTAGTGATATACACTAGTGTCTATATATATAGTTTAAACCCCAACTTGGCAATGAA	1800
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Db	2101	CAGTAACTTGTTATTGGCACTGCAACTTCTTATTGATTAATCAGGCAGGAGGAAGAAAC	2160
Qy	2161	CTTGGCACAGTATCAACTTTTGATGTGCACATGATGATTTTACACTGGCTGATTTGGTAA	2220
Db	2161	CTTGGCACAGTATCAACTTTTGATGTGCACATGATGATTTTACACTGGCTGATTTGGTAA	2220
Qy	2221	CATATAATAAGAAGTACAAATTTACCAATGGGGAGAAACAACAGAGATGGAGAAAAATCACA	2280
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Qy	2281	ATCTTAGCTGGAAATTTGGGGAGAAAGAGAAATTCGCAAGATTTCTCTCAAAAGATTTGA	2340
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Qy	2341	GGAAGAGCAGATCGCAATTTCTTTGTTGTCATGTTTCTCAAGGAGTTTCCAAATGT	2400
Db	2341	GGAAGAGCAGATCGCAATTTCTTTGTTGTCATGTTTCTCAAGGAGTTTCCAAATGT	2400
Qy	2401	TCTACATGGGTGATGAATATGGCCACACAAAAGGGGCCAACACAATACATACCTGCCATG	2460
Db	2401	TCTACATGGGTGATGAATATGGCCACACAAAAGGGGCCAACACAATACATACCTGCCATG	2460
Qy	2461	ATTCTTATGTCAATTTATTTTCGCTGGGATTAATAAGAACACATCTCTGAGTTGCACCGAT	2520
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Qy	2521	TCTGCTGCCTCATGACCAAAATTCGCAAGGAGTCCGAGGGTCTTTGGCCTTTGAGACCTTTC	2580
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Qy	2581	CAACGGCCAAACGGCTGAGTGGCATGGTCAATAGCCCTGGGAAGCCTGATTTGCTTGAGA	2640
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Qy	2641	ATAGCCGATTCGTTTGCCTTTTCCATGAAAGATGAAGACAGGGCGAGATCTATGTGGCCCT	2700
Db	2641	ATAGCCGATTCGTTTGCCTTTTCCATGAAAGATGAAGACAGGGCGAGATCTATGTGGCCCT	2700
Qy	2701	TCAACAACAGCCAATTACCGGCCCTTTGTTGAGCTTCCAGAGCGCGCAGGCGCGGTGGG	2760
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RESULT 2	REFERENCE
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LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	FEATURES
VERSION	source
KEYWORDS	
SOURCE	ORIGIN
ORGANISM	

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Qy	121	AGGACGAGCGGTGGCGAGACAGGTACGCGCTGCGCGGCGCGTGCAGGGTGCTCGCGG	180	
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Qy	181	GAATGCCGCGCGCTGGGCGCCACCGCTCGCGCGGGGTCAATTTCCGCGTCTATT	240	
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Qy	241	CCGCGGAGCACCGCGCGCGGCTGCTGCTCTTTCACGCCAGAGATCTCAAGCGCGTGG	300	
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Qy	301	GGTTGCCCTCCGAGTAGAGTTCATCAGCTTTTGGTGCGCGCGGCCCTTTTTTGGGCC	360	
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Qy	601	TATGGTGTTCAGGCGGTGTAAACAATTCGTGGCTCAGATGGCTGGCATGATCCCTCTTT	660
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Qy	661	CCATATAGCAGCTTTGATTTGGGAAGGCGACCTACTCTTAAGATATCTCTCAAAAGGACCTG	720
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Qy	841	TGTAATGAAATTAAGTCCCTGCCATGAGTTCAAACAGCTGGAGTACTCAACTCTTCTTCC	900
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Qy	1081	GGTAATGAGAAATGTCGAATTAATCATTTAAAGGGGTGCAATAATCATACTATATG	1140
Db	1081	GGTAATGAGAAATGTCGAATTAATCATTTAAAGGGGTGCAATAATCATACTATATG	1140
Qy	1141	CTTCGACCCCAAGGAGAGTTTATAAATTTCTGCTGTGGGAATACCTTTCAACTGTAAAT	1200
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Db	1201	CATCCTGTGGTTCGTCAATTCATTTAGATTTGTTTAAAGTACTGGGTGACGGAAATGCAT	1260
Qy	1261	GTTCATGTTTTTCCGTTTTTGATCTTTGCATCCATATGACAGAGTTCAGTCTGTGGAT	1320
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RESULT 3
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LOCUS Triticum aestivum partial precursor RNA for isoamylase (iso-1b
DEFINITION Gene).
ACCESSION AJ307689
VERSION AJ307689.1 GI:14331017
KEYWORDS iso-1b gene; isoamylase.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 Genschel,U., Gernot,A., Lorz,H. and Luetticke,S.
The sugary-type isoamylase in wheat: tissue distribution and
subcellular localisation
Online Publication
Planta, DOI 10.1007/s00425-001-0691-3
REFERENCE
2 Genschel,U., Abel,G., Lorz,H. and Luetticke,S.
The sugary-type isoamylase in wheat
Unpublished
3 (bases 1 to 2997)
JOURNAL Direct Submission
AUTHORS Luetticke,S.
TITLE Submitted (05-JUN-2001) Luetticke S., Insitut fuer Allgemeine
Botanik, Universitaet Hamburg, Ohnhorststrasse 18, Hamburg, 20609,
GERMANY
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2997; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AF438328 2590 bp mRNA linear PLN 13-NOV-2001
LOCUS
DEFINITION
Triticum aestivum isoamylase precursor, mRNA, complete cds;
alternatively spliced.
ACCESSION
AF438328
VERSION
AF438328.1 GI:16905062
KEYWORDS
SOURCE
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 2590)
Nethan,S., Khandelwal,R.L. and Chibbar,R.N.
AUTHORS
Characterization of isoamylase transcripts produced during wheat
TITLE
grain development and germination
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2590)
Nethan,S., Khandelwal,R.L. and Chibbar,R.N.
AUTHORS
Direct Submission
TITLE
Submitted (22-OCT-2001) Plant Biotechnology Institute, 110
JOURNAL
Gymnasium Place, Saskatoon, SK S7N 0W9, Canada
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LOCUS

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DEFINITION Triticum aestivum isoamylase wDBE-D1 mRNA, complete cds.
ACCESSION AF548380
VERSION AF548380.1 GI:31096627
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM

REFERENCE 1 (bases 1 to 2574)
AUTHORS Rahman, S., Nakamura, Y., Li, Z., Clarke, B., Fujita, N., Mukai, Y., Yamamoto, M., Regina, A., Tan, Z., Kawasaki, S. and Morell, M.
TITLE The sugary-type isoamylase gene from rice and Aegilops tauschii: characterization and comparison with maize and Arabidopsis
JOURNAL Genome 46 (3), 496-506 (2003)
REFERENCE 2 (bases 1 to 2574)
AUTHORS Rahman, S., Li, Z., Clarke, B., Regina, A. and Morell, M.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2002) Plant Industry, CSIRO, Clunies Ross, Canberra, ACT 2615, Australia

FEATURES
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RESULT 7

AX010486

LOCUS

DEFINITION

Sequence 6 from Patent WO9958690.

ACCESSION

AX010486

VERSION

AX010486.1

GI:9997329

KEYWORDS

Triticum aestivum (bread wheat)

SOURCE

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

REFERENCE

1. Luettticke, S., Abel, G., Loerz, H. and Genschel, U.

AUTHORS

Luettticke, S., Abel, G., Loerz, H. and Genschel, U.

TITLE

Nucleic acid molecules which code for enzymes derived from wheat and which are involved in the synthesis of starch

JOURNAL

Patent: WO 9958690-A 6 18-NOV-1999;

LUTTTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE); GENSCHEL ULRICH (DE); HOECHST SCHERING AGREVO GMBH (DE)

FEATURES

Location/Qualifiers

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CDS

Query Match 53.8%; Score 1611.8; DB 6; Length 2437;

Best Local Similarity 77.5%; Pred. No. 9.4e-306;

Matches 2293; Conservative 0; Mismatches 36; Indels 629; Gaps 3;

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Qy 64 CGAGGTGTGCGCGCGCGGTGTGCGAGCGCGGCGAGAGGTAGAGGACGAGGGAGGAGG 123

Db 71 CGAGGTGTGCGCGCGCGGTGTGCGAGGTGCGGCGAGGAGCGCGGAGGTGAGGGGAGGAGG 130

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Qy	2464	CTTATGTCATATTTTCGCTGGGATAAAAAGAAACATFCTCTGAGTTGTCACCGATTCT	2523
Db	1844	CTTATGTCATATTTTCGCTGGGATAAAAAGAAACATFCTCTGAGTTGTCACCGATTCT	1903
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Db	2322	AATAATATGCTATATGTA	2340
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DEFINITION	Hordeum vulgare isoamylase mRNA, complete cds.		
ACCESSION	AF490375		
VERSION	AF490375.1 GI:21314274		
KEYWORDS			
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Hordeum vulgare subsp. vulgare		
REFERENCE	1 (bases 1 to 2495)		
AUTHORS	Burton, R.A., Jenner, H., Carrangis, L., Fahy, B., Fincher, G.B., Hylton, C., Laurie, D.A., Parker, M., Waite, D., van Wegen, S., Verhoeven, T. and Denyer, K.		
TITLE	Starch granule initiation and growth are altered in barley mutants that lack isoamylase activity		
JOURNAL	Plant J. 31 (1), 97-112 (2002)		
MEDLINE	22096154		
PubMed	12100486		
REFERENCE	2 (bases 1 to 2495)		
AUTHORS	Burton, R.A., Denyer, K. and Fincher, G.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-MAR-2002) Plant Science, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia		

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Qy	478	CTGACCAACATGCTTTACGGGTACAGGTTCGACGGGACCTTGTCTCTCACTCGGGCAC 537
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RESULT 9
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LOCUS Hordeum vulgare hvisol gene for isoamylase, complete cds.
DEFINITION AB074189
ACCESSION AB074189
VERSION AB074189.1 GI:16923278
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1
AUTHORS Komatsu, A., Kato, T. and Komae, K.
TITLE Isolation of isoamylase gene in barley
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 2584)
AUTHORS Komatsu, A. and Komae, K.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2001) Akira Komatsu, National Institute of Crop
Science, Laboratory of Wheat and Barley Quality, 2-1-18 Kannondai,
Tsukuba, Ibaraki 305-8518, Japan (E-mail: akomatsu@naro.affrc.go.jp,
URL: http://nics.naro.affrc.go.jp/, Tel: 81-298-38-8945,
Fax: 81-298-38-8949)
FEATURES
Location/Qualifiers
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Best Local Similarity 75.6%; Pred. No. 6.4e-286;
Matches 2238; Conservative 0; Mismatches 92; Indels 632; Gaps 4;

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QY 118 AGGAGGACGAGCGGTGGCGAGGACAGGTACGCGCTCGCGCGCGCTGCGAGGTCGTCG 177
Db 293 AGGAGGAGGCGGTGGCTGAGGACAGGTATGCGCTCGGAGGCGCGTGCAGGGTCTCG 352
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Db 353 CCGGAATGCCCGCGCGCTGCGCGCGCCACCGCGCTCGCGCGCGGTCAATTTCCCGCT 412
QY 238 ATTCCGCGGAGGACACCGCGCGCGCTGCGCTTTCACGCCAAGAATCTCAAGCGG 297
Db 413 ACTCAGGCGGAGGACACCGCGCGCTGCGCTTTCACGCCAAGAATCTCAAGCGG 470
QY 298 TGGGGTTGCTTCCGAGTAGAGTTTCATCAGCTTTTCGCGCGCGCGCGCTTTTGG 357
Db 471 ----- 470

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QY 478 CTGCACAAATGCTTTACGGGTACAGGTTTCGACGCGACCTTTGCTCTCTCACTCGCGGAC 537
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QY 538 TACCTTGATGTTTCCATGTCGTGGTGCATCTTATGTAAGGACGTATGAAGCGGAGG 597
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QY 598 GAGTATGTTTCCAGCGCGGTGTAACAAATGCTGGGCTCAGATGGGTGGCATGATCCCT 657
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1967 ATACATACCTGCCATGATCTTATGTCATTAATTTTTCGCTGGGATAAAAAAGAGAACACT 2026
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RESULT 11

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AF142589
LOCUS AF142589 1708 bp mRNA linear PLN 12-AUG-1999
DEFINITION Hordeum vulgare isoamylase 1 mRNA, partial cds.
ACCESSION AF142589
VERSION AF142589.1 GI:4929174
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1708)
AUTHORS Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.
TITLE Analyses of isoamylase gene activity in wild-type barley indicate
its involvement in starch synthesis
JOURNAL Plant Mol. Biol. 40 (3), 431-443 (1999)
MEDLINE 9934538
PUBMED 10437827
REFERENCE 2 (bases 1 to 1708)
AUTHORS Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.
TITLE Direct Submission
JOURNAL Submitted (13-APR-1999) Plant Biology, Genetic Center, The Swedish
University of Agricultural Sciences, P.O. Box 7080, Uppsala
S-75007, Sweden

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FEATURES

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ORIGIN

Query Match 39.1%; Score 1171.6; DB 8; Length 1708;

Query Match	96.5%	Score	171.0	Length	2000
Best Local Similarity	96.5%	Pred. No.	2.2e-219		
Matches 1198; Conservative	0;	Mismatches	44;	Indels	0;
Matches 1198; Conservative	0;	Mismatches	44;	Indels	0;

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198	DB	GCATGTCTTCCTCGAAGCGGAGCTGCACGGCATGCTTTATGGGTACAGGTTTCAGCGGCAC	257
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576	QY	TAAAGCAGTGATAAAGCCGAGGGAGTATGGTGTCCAGCGCGTGGTAAACAATTTCTCGGCC	635
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636	QY	TCAGATGGCTGGCATGATCCCTCTCCATATAGCAGCTTTGATTTGGAAGGCGACCTATCC	695
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498	DB	GCATGATTCGAAGCAATGTAGAACATCCGGGTACTTTTCATTTGGGCGTGTGTCGAAGCTTGA	557
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618	DB	GCTGGAGTATGCAACCTCTTCTTCAAGATGAACCTTTTGGGGATATTTCTACCATAAACTT	677
936	QY	CTTTTTCACCAATGACAAGATACACATCAGCGCGGATAAAAACTGTGGGCGTGCATGCCAT	995
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858	DB	GGTTGATAATACTACATACCTATATGTTGCACCAAGGGAGAGTTTTATAACTATTCTGG	917
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978	DB	AAGATAGTGGGTGATGGAATGCATATGATGTTTTTCGTTTTGATCTTCATCCATAAT	1037
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Best Local Similarity 92.4%; Pred. No. 4.7e-212;
Matches 1246; Conservative 0; Mismatches 3; Indels 100; Gaps 1;

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DB 238 TCGGCGAGGTGTGCGCGCGGCTGTGAGGCGGCGACCAAGGTAGAGGACGAGGGGAGG 297
QY 121 AGGACGAGCGGTGCGGCGAGGACAGGTACGGCTTCGGCGCGGCTGCGAGGGTGTCTGCCG 180
DB 298 AGGACGAGCGGTGCGGCGAGGACAGGTACGGCTTCGGCGCGGCTGCGAGGGTGTCTGCCG 357
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DB 358 GAATGCCCGCGCGCTGGCGGCGACCGCGCTTCGGCGCGGCTCAATTTCCGCGCTTATT 417
QY 241 CCGCGGAGCGACCGCGCGCGCTTCGCTCTTTCAGCCAGAGATCTCAAGCGCGGTGG 300
DB 418 CCGCGGAGCGACCGCGCGCGCTTCGCTCTTTCAGCCAGAGATCTCAAGCGCGGTGG 472
QY 301 GGTTCCTCCGAGTAGAGTTCATCAGCTTTGCGTGGCGCGCGCGCTTTTGGGCC 360
DB 473 ----- 472
QY 361 TGCAATTAAGTTTGTACTGGGCAAAATGTCAGGATAGGCTGACCGAGGAGTTCC 420
DB 473 -----GGATAGGCTGACCGAGGAGTTCC 497
QY 421 CTTGACCCCTGATGAATCGACCGGAAAGTGTGGCATCTTTCATCGAAGCGGAGCTG 480
DB 498 CTTGACCCCTGATGAATCGACCGGAAAGTGTGGCATCTTTCATCGAAGCGGAGCTG 557
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QY 541 CTTGATGTTTCCAAATGCGTGGTGAATCTTATGCTAAGCAGTGTAAAGCCGAGGGAG 600
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DB 678 TATGGTCTCCAGCGCTGTACAAATGCTGGCTCAGATGCTGGCATGATCCCTCTT 737
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DB 858 CCGGGTACTTTCATTGAGCTGTGTCAAGCTTGACTATTGAGGAGCTTGAGGTTAAT 917
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DB 918 TGTATTGAATTAATGCCCTGCCATGAGTCAACGAGCTGAGTCAACCTCTTCTTCC 977
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RESULT 13
AB015615
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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AB015615
AB015615.1 GI:3252793
isoamylase.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
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Fujita,N., Kubo,A., Francisco,P.B. Jr., Nakakita,M., Harada,K.,
Minaka,N. and Nakamura,Y.
Purification, characterization, and cDNA structure of isoamylase
from developing endosperm of rice
Planta 208 (2), 283-293 (1999)
99266133
MEDLINE
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PUBMED

REFERENCE
2 (bases 1 to 2288)
Nakamura,Y.
Direct Submission
Submitted (17-JUN-1998) Yasunori Nakamura, National Institute of
Agricultural Resources, Department of Plant Physiology; 2-1-2
Kannonndai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:nakayn@abr.affrc.go.jp, Tel:81-298-38-8382,
Fax:81-298-38-8347)

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ORIGIN

Query Match 36.7%; Score 1101.2; DB 8; Length 2288;
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Matches 1923; Conservative 0; Mismatches 273; Indels 628; Gaps 3;

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Qy	660	TCCATATAGCACGTTTGAATGGGAGCGACCTACCTTAAGATATCTCTCAAAAGGACCT	719
Db	441	TCCGATACGATACGTTTGAATGGGAGCGACCTACCTTAAGATATCTCTCAAAAGGACCT	500
Qy	720	GGTAATATAGATGACATGCTGCTGATTCAGAACGATGATTCAGCAATGCTAGAAC	779
Db	501	TGTAATATAGATGACATGCTGCTGATTCAGAACGATGATTCAGCAATGCTAGAAC	560
Qy	780	TCCGGGTACTTTCATTTGAGGTGTGTCTGAAAGCTTGACTATTTGAAGGAGCTTGGAGTTAA	839
Db	561	TCCAGGACCTTACATTTGGGCTATATCAAAAGCTTGACTATCTGAAGGAGCTTGGAGTTAA	620
Qy	840	TTGTATTGAATTATGCTGCTGATGTTCAAGGAGTGGAGTACTCAACCTCTCTTC	899
Db	621	CTGTGTAGATTGATGCTGCTGATGTTCAAGGAGTGGAGTACTCAACCTCTCTTC	680
Qy	900	CAAGATGAATTTTGGGGATTTTACCATAAATCTTTTCCACCAATGACAGATACAC	959
Db	681	CAAGATGAATTTTGGGGATTTTCCAGATAAATCTTTTCCACCAATGATAGATATTC	740
Qy	960	ATCAGGCGGGATAAAATCTGTTGGGCTGATGCTCAATTAATGAGTTCAAACTTTTGAAG	1019
Db	741	ATCAGGCGGGATAAAATCTGTTGGGCTGATGCTCAATTAATGAATTTCAAACTTTTGTAG	800

Qy	1020	AGAGGCTCACAAACGGGGAATTTAGGTGATCCCTGGATGTTGTCTTCAACCATACAGCTGA	1079
Db	801	AGAGGCTCACAAACGGGGAATTTAGGTGATCATGGATGTTGTCTTCAATCATACAGCGGA	860
Qy	1080	GGGTAATCAGAAATGGTCCAAATTTATCATTTTAAAGGGGTGATTAATACTACATCATATAT	1139
Db	861	GGGTAATCAGAAAGGACCAATTTATCATTTTAAAGGGATAGATAATAGCACATCATATAT	920
Qy	1140	GCTTGACCCCAAGGAGAGATTTTATACTATTCTGGCTGTGGGATACCTTCAACTGTAA	1199
Db	921	GCTTGACCCCTAAGGAGAGATTTTACAATTTCTGGTGTGGGATACCTTCAACTGTAA	980
Qy	1200	TCATCTCTGTGTTCTGTCATTTCAATTTAGTATTGTTTAAAGTACTGGGTGACGGAATGCA	1259
Db	981	TCATCTCTGTGTTCTGTCATTTTATTTAGTATTGTTTAAAGTACTGGGTGACGGAATGCA	1040
Qy	1260	TGTTGATGGTTTTCTGTTTGTGATTTGATTCATTAATGACAGAGGTTCCAGTCTGTGGGA	1319
Db	1041	TGTTGATGGTTTTCTGTTTGTGATTTTATTTAGTATTGTTTAAAGTACTGGGTGACGGAATGCA	1100
Qy	1320	TCCAGTTAAACGTGTATGAGCTCCAAATAGAAAGTGACATGATCAACAACAGGACACCTCT	1379
Db	1101	TCCAGTTAAATGTATGAAAGTCCAGTAGAAGTGACATGATGATGACGAGGACACCTCT	1160
Qy	1380	TGTTACTCCACACTTATTTGATCATGATCAGCAATGACCAATTTCTGGAGCGTCAAGCT	1439
Db	1161	TGTTACTCCACACTTATTTGATCATGATCAGCAATGATCAGCAATTTCTGGAGATGTCAAGCT	1220
Qy	1440	CATTGCTCAAGCATGGGATGAGGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGAA	1499
Db	1221	CATTGCTCAAGCATGGGATGAGGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGAA	1280
Qy	1500	TGTTTGGTCTGAGTGGAAATGGAAAGTACCGGAGCATTTGCGTCAATTCATTAAGGCAC	1559
Db	1281	AAATTTGGTCAAGATGGAAATGGAAAGTACCGGAGCATTTGCGTCAATTCATTAAGGCAC	1340
Qy	1560	TGATGATTTGCTGGTGGTTTTGCGGAATGTTTGTGGAAAGTCCACACTATACAGGT	1619
Db	1341	AGATGATTTGCTGGTGGTTTTGCGGAATGTTTGTGGAAAGTCCACACTATAC	1395
Qy	1620	AAGTTGTGCAATCTTGTAAATGATGTTGAGTGAATGTCACTGGATTTTATATATAC	1679
Db	1396	-----	1395
Qy	1680	CACATGATGATACACATCTAAATATATAAACAATCATAGTGTATGCATATGCAATTTGGCTA	1739
Db	1396	-----	1395
Qy	1740	AGAAGTATTAGTGTATACACTAGTGTCTATATATAGTTTAAACCCCAACTTGCCAATGA	1799
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Qy	1800	AGGAACATAGGGCTTCTAGTATCTTATTTATTTGTCGGGTGAATAATCCACTGAAAA	1859
Db	1396	-----	1395
Qy	1860	TTCCAGCCATGTCATTTTATAGGGGGGAGAGAACTATATTGATTTGCCCCCTTAAA	1919
Db	1396	-----	1395
Qy	1920	GAAAGCATCTCAGAAATTCATAGTAAGTTGCTTTCTGTAAAGAAAGGAAACGACTTCA	1979
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Qy	1980	TACTTTCTATCGGTCTAACTTAGCTCGATGTATATTGTGAAGATGAATGCCAATTTAA	2039
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Qy	2040	TTTGTGGATTAATTGATCTGTATTTCACAAATTTCTATTTGGTTTCTCTAGAAATCAAA	2099
Db	1396	-----	1395

Db 541 GCTCCAAATAGAGGTGATGATCAACAAGGGACACCTCTTGTACTCCACCATTATT 600
Qy 1399 GACATGATCAGCAATGACCAATTTCTTGGAGGGCTCAAGCTCATTTGCTGAAGCATGGAT 1458
Db 601 GACATGATCAGCAATGACCAATTTCTTGGAGGGCTCAAGCTCATTTGCTGAAGCATGGAT 660
Qy 1459 GCAGGAGCCCTCATCAAGTAGTCAATTCCTTCACTGGAAATGTTTGGTCTGAGTGGAT 1518
Db 661 GCAGGAGCCCTCATCAAGTAGTCAATTCCTTCACTGGAAATGTTTGGTCTGAGTGGAT 720
Qy 1519 GGGAAATGACGGGACATTTGCGCTCAATTCATTTAAAGGCACTGATGATTTGCTGGTGT 1578
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Qy 1579 TTTGCCGAATGCTTTTGTGGAAGTCCACCTTATACAGGTAAGTTGTGGCAATCTTGT 1638
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Db 817 ----- 816
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Qy 1759 CTAGTGTATATAGTGTATTAACACCACTTTGCCAATGAAGGAACATAGGCTTTCTA 1818
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Qy 1939 TAGTAAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCTATCTTTCTATCGTGCTAA 1998
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Qy 2179 TTGTATGTGCATGATGATTTACATGCTGCTGATTTGGTAAACATATATAGAAATCA 2238
Db 854 TTGTATGTGCATGATGATTTACATGCTGCTGATTTGGTAAACATATATAGAAATCA 913
Qy 2239 ATTTTACAAATGGGGAGAAACACAGAGATGGAGAAATCAATCTTTAGCTGGAATTTGT 2298
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Qy 2359 ATTTCTTTGTTGCTCATGTTTCTCAAGAGTTTCAATGTTTCTACATGGGTGATGAAT 2418
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Qy 2599 AGTGGCATGTCATCAGCTCGGGAAGCCTGATTGGTCTGAGATAGCCGATTGTTGCCT 2658
Db 1274 AGTGGCATGTCATCAGCTCGGGAAGCCTGATTGGTCTGAGATAGCCGATTGTTGCCT 1333
Qy 2659 TTTCCATGAAGATGAAGACAGGCGGAGATCTATGTGGCTTCCAAACAGCCAGCCACTTAC 2718
Db 1334 TTTCCATGAAGATGAAGACAGGCGGAGATCTATGTGGCTTCCAAACAGCCAGCCACTTAC 1393
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Db 1454 GCAAGCCAGCACCATAGACTTCTCCTCACGACGACTTACCTGATCGCGCTCTCACCATAC 1513
Qy 2839 ACCAGTTCTCGCATTTCTCTACTTCCAACTCTACCCCATGCTCAGCTACTCATCGTCA 2898
Db 1514 ACCAGTTCTCTCTCTTCTCTCACTTCCAACTCTACCCCATGCTCAGCTACTCATCGTCA 1573
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Qy 2959 TGTA 2962
Db 1634 TGTA 1637

RESULT 15

AR427894
LOCUS AR427894 2700 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15 from patent US 6639126.

ACCESSION AR427894
VERSION AR427894.1 GI:40186914

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2700)

AUTHORS Sewalt,V.J.H. and Singletary,G.W.

TITLE Production of modified polysaccharides

JOURNAL Patent: US 6639126-A 15 28-OCT-2003;

FEATURES Location/Qualifiers

source 1..2700

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 33.6%; Score 1008; DB 6; Length 2700;
Best Local Similarity 65.9%; Pred. No. 3.1e-187;
Matches 1888; Conservative 0; Mismatches 345; Indels 633; Gaps 4;

Qy 79 CGGTGTGTCAGCGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138
Db 233 CGGTGCGCGCGCGGTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 292
Qy 139 AGGACAGGTACCGCTCGGCGCGCGCTGACGGGTGCTCGCGGGAATGCCCGCGCGTGG 198
Db 293 AGGAGAGGTTCCGCTGGCGCGCGGTGCCGGGTGCTCGCGGGAATGCCCGCGCGTGG 352
Qy 199 GCGCCACCGCTCGCGCGCGGTCAATTTCCGCGCTTATTCGCGGAGGAGGAGGAGGAGG 258
Db 353 GCGCCACCGCTCGCGCGCGGTGTCAATTTCCGCGTCTACTCGCGGTGCTTCCCGCGG 412

[illegible]

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 Db 1621 AGTTGTGGCAATACCTTGTAATGAGTTGAGTGAATGTCACTGGATTTTATATATATACC 1680
 Qy 1681 ACATGATGATACACATCATTAATATATAAACAATCATAGTGTATGTCATATGCTTAA 1740
 Db 1681 ACATGATGATACACATCATTAATATATAAACAATCATAGTGTATGTCATATGCTTAA 1740
 Qy 1741 GAAGTATTAGTATACACTAGTGCCTATATATAGTGTTCGCGTGAATATCACTGGAAT 1800
 Db 1741 GAAGTATTAGTATACACTAGTGCCTATATATAGTGTTCGCGTGAATATCACTGGAAT 1800
 Qy 1801 GBAACATAGGCTTCTAGTATCTTATTTATTTGTCGCGTGAATATCACTGGAAT 1860
 Db 1801 GBAACATAGGCTTCTAGTATCTTATTTATTTGTCGCGTGAATATCACTGGAAT 1860
 Qy 1861 TCCAGCCATGTCAATTTTATAGGCGGGGAGAGAACTATATTTGTCGCGCTTAAAG 1920
 Db 1861 TCCAGCCATGTCAATTTTATAGGCGGGGAGAGAACTATATTTGTCGCGCTTAAAG 1920
 Qy 1921 AAGCATCTCAGAAATCATAGTAAAGTTAGTGTCTTTCTGTAAGAAAGAAACGACTTCAT 1980
 Db 1921 AAGCATCTCAGAAATCATAGTAAAGTTAGTGTCTTTCTGTAAGAAAGAAACGACTTCAT 1980
 Qy 1981 ACTTTCATCGGTCTAACTTAGCTCATATATTTGTAAGATGAATGCCAAATTTAAT 2040
 Db 1981 ACTTTCATCGGTCTAACTTAGCTCATATATTTGTAAGATGAATGCCAAATTTAAT 2040
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 Db 2041 TTGTCGGAATTTGATCTGTTATTCACAAATTTCTATTTGTTTCTCTAGAAATCAAC 2100
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 Db 2101 CAGTAACCTGTATTTGCACTGCACTTCTATTTGTAATCAGGAGGAGGAGAAAC 2160
 Qy 2161 CTGGCACAGTATCAACTTTGTATGTGCATCATATGATGATTTACACTGGCTGATTTGGTAA 2220
 Db 2161 CTGGCACAGTATCAACTTTGTATGTGCATCATATGATGATTTACACTGGCTGATTTGGTAA 2220
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 Db 2221 CATATATAGAAGTACAAATTTACCAATTTGGGAGAACACACAGATGAGGAAATCACA 2280
 Qy 2281 ATCTTAGCTGAATTTGGGAGGAGGAGAAATTCGCAAGATTTCTGTCAAAAGATTGA 2340
 Db 2281 ATCTTAGCTGAATTTGGGAGGAGGAGAAATTCGCAAGATTTCTGTCAAAAGATTGA 2340
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 Db 2341 GGAAGAGGAGATCGGCAATTTCTTTGTTGTCATGTTCTCAAGGAGTTCCAAATGT 2400
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 Db 2401 TCTACATGGGTGATGAATATGGCCACACAAAGGGGCAACAATACATACATCTGCCATG 2460
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 Db 2461 ATTCTTATGTCAATTTTTCGTTGGATATAAAGAAACAATCTCTGAGTTCCACCGAT 2520
 Qy 2521 TCTGCTGCTCATACCAATTCGCAAGGATGCGAGGGTCTTGGCTTTGAGGACTTTC 2580
 Db 2521 TCTGCTGCTCATACCAATTCGCAAGGATGCGAGGGTCTTGGCTTTGAGGACTTTC 2580
 Qy 2581 CAACGGCCAAACGGCTGAGTGGATGCTCATCAGCTGGGAAAGCTGATTTGTTCTGAGA 2640
 Db 2581 CAACGGCCAAACGGCTGAGTGGATGCTCATCAGCTGGGAAAGCTGATTTGTTCTGAGA 2640
 Qy 2641 ATAGCCGATTCGTTGCTTTTCCATGAAAGTGAACACAGGCGGAGATCTATGTGSCCT 2700
 Db 2641 ATAGCCGATTCGTTGCTTTTCCATGAAAGTGAACACAGGCGGAGATCTATGTGSCCT 2700

Qy 2701 TCAACACAGCCACTTACCGGCGCTTGTGAGCTCCAGAGCGCGCAGGCGCGGTGGG 2760
 Db 2701 TCAACACAGCCACTTACCGGCGCTTGTGAGCTCCAGAGCGCGCAGGCGCGGTGGG 2760
 Qy 2761 AACCGGTGGTGGACACAGCGCAAGCCAGCACCATACGACTTCTCACCAGACGACTTACCTG 2820
 Db 2761 AACCGGTGGTGGACACAGCGCAAGCCAGCACCATACGACTTCTCACCAGACGACTTACCTG 2820
 Qy 2821 ATCGGCTCTCACCATACACAGCTCTCGGATTTCTTACTCTCAACTCTACCCATGC 2880
 Db 2821 ATCGGCTCTCACCATACACAGCTCTCGGATTTCTTACTCTCAACTCTACCCATGC 2880
 Qy 2881 TCAGCTACTCATCGGTCTATCTAGTATTGCGCCCTGATTTTGAGAGACCAATATATACA 2940
 Db 2881 TCAGCTACTCATCGGTCTATCTAGTATTGCGCCCTGATTTTGAGAGACCAATATATACA 2940
 Qy 2941 GTAATAATATGCTCTATATGTATAAATAAATAAATAAATAAATAAATAAATAAATAA 2997
 Db 2941 GTAATAATATGCTCTATATGTATAAATAAATAAATAAATAAATAAATAAATAAATAA 2997

RESULT 2 AAX34654

ID AAX34654 standard; cDNA; 1706 BP.

XX AAX34654;

AC AC

XX 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

XX Partial cDNA for hexaploid wheat DBE.

XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
 KW grain softness protein 1; bacterial isoamylase; glycogen synthase;
 KW WBE I-D4 gene; ss.

XX Aegilops tauschii.

OS Location/Qualifiers

XX 1..1704

FT /*tag= a

FT /note= "partial DBE; the attr and stop codons are not

FT indicated"

XX WO9914314-A1.

XX 25-MAR-1999.

XX 11-SEP-1998; 98WO-AU0000743.

XX 12-SEP-1997; 97AU-00009108.

XX 20-MAR-1998; 98AU-00002509.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (AUSU) UNIV AUSTRALIAN NAT.

XX (GOOD-) GOODMAN FIELDER LTD.

XX (LINA-) GRP LINAGRAIN PACIFIC PTY LTD.

XX Li Z, Morell M, Rahman S;

XX WPI; 1999-229525/19.

XX P-PSDB; AAY06918.

XX New isolated cereal plant enzyme genes used for, e.g. expression of

XX antisense sequences of granule bound synthase.

XX Claim 47; Page 100-102; 17pp; English.

XX The invention relates to a novel enzyme of starch biosynthetic pathway in

XX a cereal plant, where the enzyme is selected from starch branching enzyme

CC

CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
 CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
 CC rice or maize. The methods and products can be used for targeting
 CC expression specifically to the endosperm of the seeds of cereal plants
 CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.
 CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the wheat DBE partial cDNA sequence. (Updated
 CC on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1706 BP; 467 A; 355 C; 415 G; 469 T; 0 U; 0 Other;

Query Match 35.8%; Score 1074.4; DB 2; Length 1706;
 Best Local Similarity 74.9%; Pred. No. 6.6e-222;
 Matches 1621; Conservative 0; Mismatches 16; Indels 527; Gaps 1;

QY 799 GCTGTGCGAAGCTTGACTATTTCGAAGAGCTTGGAGTTAAATGTAATTAATGCCCC 858
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QY 859 TGCCATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCTCCAGAGTGAACCTTTGGGGA 918
 DB 61 TGCCATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCTCCAGAGTGAACCTTTGGGGA 120

QY 919 TATTTACCAATAAATCTTTTTCACCAATGACAAGATACACATCAGCGGGGATAAAAAAC 978
 DB 121 TATTTACCAATAAATCTTTTTCACCAATGACAAGATACACATCAGCGGGGATAAAAAAC 180

QY 979 TGTGGGCGTGATGCCATAAATAGATTCAAACTTTTGTAAAGAGAGCTCAAAACCGGGA 1038
 DB 181 TGTGGGCGTGATGCCATAAATAGATTCAAACTTTTGTAAAGAGAGCTCAAAACCGGGA 240

QY 1039 ATTGAGGTGATCCGTGATGTTGCTTCAACATACAGCTCAGAGTAAATGAGATGTCCA 1098
 DB 241 ATTGAGGTGATCCGTGATGTTGCTTCAACATACAGCTCAGAGTAAATGAGATGTCCA 300

QY 1099 ATATTATCAATTAAGGGGTCGATAATACATACATATATGTTGCACCCAGGGAGAG 1158
 DB 301 ATATTATCAATTAAGGGGTCGATAATACATACATATATGTTGCACCCAGGGAGAG 360

QY 1159 TTTTATAACTATCTGCTGCGGATACCTTCACTGTAATCATCTGCTGCTGCTCA 1218
 DB 361 TTTTATAACTATCTGCTGCGGATACCTTCACTGTAATCATCTGCTGCTGCTCA 420

QY 1219 TTCAATTGATGTTTAAAGATACCTGGGTGACGGAAATCATGTTGATGTTTTCGTTTT 1278
 DB 421 TTCAATTGATGTTTAAAGATACCTGGGTGACGGAAATCATGTTGATGTTTTCGTTTT 480

QY 1279 GATCTTGATCCATAATGACAGAGTTCCAGTCTGTGGATCCAGTTAACTGATGGA 1338
 DB 481 GATCTTGATCCATAATGACAGAGTTCCAGTCTGTGGATCCAGTTAACTGATGGA 540

QY 1339 GCTCCATAGAAGTGATCATGATCACAAAGGACACCTCTTCTTACTCCACCACATTT 1398
 DB 541 GCTCCATAGAAGTGATCATGATCACAAAGGACACCTCTTCTTACTCCACCACATTT 600

QY 1399 GACATGATCAGCAATACCAATTTTGGAGGCGTCAAGCTCATGCTGAAGCATGGAT 1458
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QY 1459 GCAGGAGCTCTATCAAGTAGTCAATTCCTCCTGGAATGTTTGGTCTGATGGAAT 1518
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 DB 721 GGGAAAGTACCGGACATTTGTCGTCAATTCATTAAGGCACTGATGGAATTTGCTGGT 780

QY 1579 TTTGCGCAATGCTTTTGGAGTCCACACCTATACAGGTAGTTGTGGCAATCTTGT 1638
 DB 781 TTTGCGCAATGCTTTTGGAGTCCACACCTATACAGGTAGTTGTGGCAATCTTGT 816

QY 1639 AAATGAGTTGAGTGAATGTACCTGGATTTTATATATATACCATGATGATACATCT 1698
 DB 817 ----- 816

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QY 1999 CTTAGCTCGATATATTGTAAGATGAATGCCAAATTTAATTTGTCGGATAAATTTGATC 2058
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 DB 854 TTGTATGTGCATGATGATTTTACATCGCTGATTTGGTAAACATATAATAAGAAATGACA 913

QY 2239 ATTTACCAATATGGGAGAACCAAGAGATGAGAGAAATCAAACTTTAGCTGGAATTTGTG 2298
 DB 914 ATTTACCAATATGGGAGAACCAATGAGATGAGAGAAATCAAACTTTAGCTGGAATTTGTG 973

QY 2299 GGGAGGAAGGAATTCGCAAGATTCTGTCAAAAGATTGAGGAAGAGGAGATGCGCA 2358
 DB 974 GGGAGGAAGGAATTCGCAAGATTCTGTCAAAAGATTGAGGAAGAGGAGATGCGCA 1033

QY 2359 ATTTCTTTGTTGTTCTCATGTTTCTCAAGAGTTCCAATGTTCTACATGGGTGATGAAT 2418
 DB 1034 ATTTCTTTGTTGTTCTCATGTTTCTCAAGAGTTCCAATGTTTACATGGGTGATGAAT 1093

QY 2419 ATGSCCAACAAAAAGGGGGCAACCAATACATCTGCCATGATTTCTATGTCAATTAAT 2478
 DB 1094 ATGSCCAACAAAAAGGGGGCAACCAATACATCTGCCATGATTTCTATGTCAATTAAT 1153

QY 2479 TTCGTGGGATAAAAAGAAACAATCTCTGAGTTGCAACGATTTCTGCTGCTCATGACCA 2538
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QY 2599 AGTGGCATGTCATCAGCTGGGAAGCTGATTTGGTCTGAGATAGCCGATTTCTTGGCT 2658
 DB 1274 AGTGGCATGTCATCAGCTGGGAAGCTGATTTGGTCTGAGATAGCCGATTTCTTGGCT 1333

QY 2659 TTTCCATGAAGATGAAGAGCAGGGCGAGATCTATGTGGCTTCAACACAGCCACTTAC 2718
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QY 2719 CGGCCGTTGTAGCTCCAGAGCGCCAGCGCGCCGCGCGCGGTGGGAACCGGTGGTGACACAG 2778
DB 1394 CGGCCGTTGTAGCTCCAGAGCGCGCGCGCGCGGTGGGAACCGGTGGTGACACAG 1453
QY 2779 GCAGCCAGCACCATTAGCTCTCTCACGACGACTTACCTGATCGGCTCTCACCATAC 2838
DB 1454 GCAGCCAGCACCATTAGCTCTCTCACGACGACTTACCTGATCGGCTCTCACCATAC 1513
QY 2839 ACCAGTTCTCGCAATTTCTCTACTTCCAACTCTACCCCATGCTCAGCTACTCATCGGTCA 2898
DB 1514 ACCAGTTCTCTCAATTTCTCTCAACTCCAACTCTAGCCCATGCTCAGCTACTCATCGGTCA 1573
QY 2899 TCCTAGTATTGGCCCTGATGTTTGAGAGACCAATATATACAGTAATATATGTTCTATA 2958
DB 1574 TCCTAGTATTGGCCCTGATGTTTGAGAGACCAATATATATACAGTAATATATGTTCTATA 1633
QY 2959 TGTA 2962
DB 1634 TGTA 1637

RESULT 3
AAI76375
ID AAI76375 standard; cDNA; 2712 BP.
XX
AC AAI76375;
XX
DT 04-AUG-1999 (first entry)
XX
DE Zea mays SU1 starch debranching enzyme encoding cDNA clone.
XX
KW Zea mays; SU1; starch debranching enzyme; maize; endosperm; corn;
XX bacterial isomylase; alpha-amylase; starch hydrolytic enzyme; sugary 1;
XX ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 1..2457
FT /*tag= a
XX
XX US912413-A.
XX
XX 15-JUN-1999.
XX
XX 24-MAR-1995; 95US-00410784.
XX
XX 24-MAR-1995; 95US-00410784.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Myers AM, James MG;
XX
XX WPI; 1999-357234/30.
XX
XX P-PSDB; AAY17523.
XX
XX SU1 starch debranching enzyme.
XX
XX Claim 3; Fig 1; 39pp; English.
XX
XX The present sequence encodes a starch debranching enzyme active in maize
XX endosperm (Zea mays), designated SU1. SU1 protein is useful as a
XX replacement for the bacterial and fungal enzymes currently used in the
XX starch processing industry
XX
XX Sequence 2712 BP; 636 A; 646 C; 745 G; 685 T; 0 U; 0 Other;
XX
XX Query Match 33.4%; Score 1000; DB 2; Length 2712;
XX Best Local Similarity 65.7%; Pred. No. 9e-206;
XX Matches 1883; Conservative 0; Mismatches 350; Indels 633; Gaps 4;
XX
XX 79 CGGTTGTCAGCGCGCAGGAGGTAGAGGACGAGGCGGAGGAGGAGCGCGGTGGCGG 138

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DB 223 CCGTGGCCGAGCGGTGCGAGCGGAGGAGGACGACGACGACGAGGAGGTGGCGG 292
QY 139 AGGACAGGTACGCGCTCGCGCGCGCGGTGCAAGGTGCTCGCGGAATGCCCGCGCGCTGG 198
DB 293 AGGACAGGTTCGCGCTCGCGCGCGCGGTGCTCGCGGAATGCCCGCGCGCTGG 352
QY 199 GGGCCACGCGCTCGCGCGCGCGGTGCAATTTTCGCGGTCTATTCGCGGAGGCCACCGCGG 258
DB 353 GGGCCACGCGCTCGCGCGCGCGGTGCAATTTTCGCGGTCTATTCGCGGAGGCCACCGCGG 412
QY 259 GGGCGCTCTGCGCTCTTCACGCGCAGAGATCTCAAGGCGGTGGGTGCTCCGAGTAGA 318
DB 413 GGTCTGAGCTCTTCGCTCCGCGGACCTCAAGGC----- 449
QY 319 GTTCATGACTTTGCGTGGCGCGCGCCCTTTTGGGCGCTGCAATTAAGTTTGTGA 378
DB 450 ----- 449
QY 379 CTGGGGCAATGCTGACGAGTAGGTGACCGAGGAGTTCCCTTGACCCCTGATGAT 438
DB 450 -----GGATAGGTGACCCGAGGAGGTGCCCTCGATCCCTGCTCAAC 492
QY 439 CGGACCGGGAACGTTGTGGCATGTCTTCATCGAAGG---CGAGCTGCACAAACATGCTTAC 495
DB 493 CGAACGGGAACGTTGTGGCATGTCTTCATCCAGGGGACGAGCTGCACGGCATGCTCTGC 552
QY 496 GGGTACAGTTTCGACGGCACCTTTGCTCTCTGCTGCGGGGACCTACCTTGATGTTTCCAAT 555
DB 553 GGATACAGTTTCGATGGCGTGTTCGCGCTGAGCGCGGACAGTACTAGATGTGTCGAAC 612
QY 556 GTCTGGTGGATCCTTATGCTAAGGCAGTGATTAAGCGAGGGGAGTATGTTTCCAGCG 615
DB 613 GTTGTGGTGGATCCTATAGCTAAGGCAGTGGTAAAGCGAGGTGATATGTTGCTGGG 672
QY 616 CCGTGTAAACAATGTTGCGCTCAGATGCTGGCATGATCCCTCTTCCATATAGCAGTTT 675
DB 673 CCGTGTGGTGGTGTGTTGGCTCAAAATGGCTGATGATCCCTCTTCCCTATAAATGTTT 732
QY 676 GATTGGGAGGCGACCTACCTCTAAGATATCTCTAAAGGAGCGTGGTATATATAGATG 735
DB 733 GATTGGGAGGCGACCTACCTCTTGGTACCATCAAGAGGACCTTGTCTATATAGAAATG 792
QY 736 CACTTGGCTGGATTCCAGGAAGCATGATTCAGCAATGTAGAACATTCGGGTACTTTCAAT 795
DB 793 CATTTGGTGGATTCCAGGAAGCACAACTCAAGCAAGACAAAACACCCAGGAACCTTACAT 852
QY 796 GGAGCTGTGCGAAGCTTGAATTTGAAGGAGCTTGGAGTTAATGTTGTAATTAATG 855
DB 853 GGTGTGTGTCAAGCTTGACCATTAAGGAACTTGGAGTGAATGATATAGAGCTAATG 912
QY 856 CCTGCGCATGATTCAACGAGCTGGAGTACTCAACCTCTTCTTCAAGATGAACCTTTTGG 915
DB 913 CCTGCGCATGATTCAAGGAGTGAATTTGAGTACTTCACTCTCTTCAAGATGAACCTTTGG 972
QY 916 GGATATTTACATAAATCTTTTTCACCAATGACAGATACATCATAGGCGGGATATAA 975
DB 973 GGATATTTACATAAATCTTTTTCACCAATGACAGATATTTCTCAAGTGGCATAAGA 1032
QY 976 RACTGTGGCGGTGATCCATTAATGATTTCAAACTTTTGTAAAGAGAGGCTCACAAACGG 1035
DB 1033 GACTCTGATGTGGTGGCATAAATTAAGCTTTTGTAAAGGAGGCGCCACAAACGG 1092
QY 1036 GGAATTTAGGTGATCCTGGATTTCTTCAACCATACAGCTGAGGGTAATGAGAAATGGT 1095
DB 1093 GGAATTTAGGTGATCATGATTTCTTCAATCATACAGCTGAAGGTAATGAGAAAGGC 1152
QY 1096 CCAATATTATCATTTAAGGGGTGATATATCTACTATATCTGCTGACCCCAAGGA 1155
DB 1153 CCAATATTATCTTTAGGGGATAGATATATAGTACTACTGCTTGCACCTAAGGA 1212
QY 1156 GAGTTTATAAATTTCTGGCTGTGGGAATACCTTCAACTGTAATCATCTCTGTGTTGGT 1215
DB 1213 GAGTTTATAAATTTCTGGTTGTGAAATACCTTCAATTTGATCATCTCTGTAGTCCGT 1272

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QY 1216 CAATTCATTGTAGATGTTTAAAGATACCTGGGTGACGAAATGATGTTGATGTTTTCGT 1275
DB 1273 GAAATTTATAGTGGATTGCTTGAGATACCTGGGTACAGAAATGATGTTGATGTTTTCGT 1332
QY 1276 TTTCATCTTGCATCCATAAGACACAGAGTTCCAGTCTGTGGGATCCAGTTAAGCTGAT 1335
DB 1333 TTTCACCTTGATCTTATCTACACAGAGATGCGAGTCTATGGGATCCAGTTAATGTTAT 1392
QY 1336 GGAGCTCCAAATGAGAGTGACATGATCACACAGGACACCTCTTGTACTCCACCACCT 1395
DB 1393 GGAAGTCCAAATGGAAGGTGACATGATTACGACAGGACACCTCTTGTGTGCCCCACCACCT 1452
QY 1396 ATTCACATGATCAGCATGACCAATTTCTGGAGCGTCAAGTCTCAATGCTGAGCATGG 1455
DB 1453 ATTTGACATGATTGCAATGACCCAAATTTCTGGAAATGTCAAGTCTCATGCTGAAGCATGG 1512
QY 1456 GATCAGAGAGCCCTCTATCAAGTAGTCAATTCCTCACTGGAATGTTTGGTCTGAGTGG 1515
DB 1513 GATCAGAGAGTCTCTATCAAGAGGTCACTTCTCACTGGAACGTTTGGTCAAGTGG 1572
QY 1516 AATGGAGTACCGGACATTTGCGTCAATTCATTAAGGACACTGATGATTTGCTGGT 1575
DB 1573 AATGGAAGTATCGCATACCGTGGTCACTTCAATCAAGGACAGATGGATTTGCTGGT 1632
QY 1576 GGTTTTGGCGAATGCTCTTTGTGGAAGTCCACACCTATACCAGGTAAAGTTGGCAATACT 1635
DB 1633 GCTTTTGTGTAAGTCTATGTTGGAAGTCCACAGTTATC----- 1671
QY 1636 TGTAATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCAATGATGATACAA 1695
DB 1672 ----- 1671
QY 1696 TCTAAATATACAAATAGTATGATGATGCAATTTGGCTAAGAGTATTAGTGAT 1755
DB 1672 ----- 1671
QY 1756 ACACGTAGTCTATATATAGTATTTTACACCCCACTTGCCAAATGAAGGAACATAGGCTTT 1815
DB 1672 ----- 1671
QY 1816 CTAGTTATCTTATTATTGTCGGTGAATTAATCCACTGAAATAATCCAGCCATGTCATT 1875
DB 1672 ----- 1671
QY 1876 TTTTAGGGGGGAGAGAACTATATTGATTGTCGCCCTTAAAGAGCCATCTCAGAAAT 1935
DB 1672 ----- 1671
QY 1936 TCATAGTAAAGTCTGCTTTCTGTAAGAAAGGAACGACTTCATCTTCTATCGGTGC 1995
DB 1672 ----- 1671
QY 1996 TAACTTAGTCGATGATATTGTAAGATGAATGCCAAATTTAATTTGTCGGATAATTG 2055
DB 1672 ----- 1671
QY 2056 ATCTGTTATTCACAAATTTCTATTGTTGTTTCTCTAGAAATCAAAACAGTAACCTTGTATT 2115
DB 1672 ----- 1671
QY 2116 GGCACTGCAACTCTTATTGTTAATCAGCAGGAGGAAGAACTTGGCACAGTATCA 2175
DB 1672 -----CAGCAGGGGGGAGGAAGCCCTTGGCACAGTATCG 1705
QY 2176 ACTTTGATGTGCATCATGGAATTACACTGGCTGATTTGGTAACATATAATAAGAAAT 2235
DB 1706 GCTTTGATGTGCACACGATGGAATTACACTGGCTGATTTGGTACATACAAATAGCAAGT 1765
QY 2236 ACAATTTACCAATGGGAGNACACAGATGAGNAAATCAATCTTAGCTGGAAT 2295
DB 1766 ACAACTTGTCAAATGGTGAAGACTTCAGATGGGAAATCATATCTTAGCTGGAAT 1825

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QY 2296 GTGGGAGGAGGAGAAATTCGCAAGATTGTCGTCAAAAGATTGAGGAAGGCGAGATGC 2355
DB 1826 GTGGGAGGAGGAGAAATTCGCAAGATTGTCGTCGAGTCCGGAAGATTGAAGGAAGGCGAAATGC 1895
QY 2356 GCAATTTCTTTGTTGTTCTCATGTTTCTCAAGAGATTCCAAATGTTCTATCATGGGTGATG 2415
DB 1886 GCAATTTCTTTGTTGTTCTCATGTTTCTCAAGAGATTCCAAATGTTCTATCATGGCGATG 1945
QY 2416 AATATGGCCACACAAAAGGGGGCAACAATACTGTCGATGATCTTATGTCAATT 2475
DB 1946 AATATGGTCAACAAGGAGGGAACAACAATAGCTACTGCTGATGACCAATTTATGTCAATT 2005
QY 2476 ATTTTCGCTGGGATAAAA---AAGAACAAATCTCTGAGTTGCACCGATTCTGCTGCCTCA 2532
DB 2006 ATTTCCGTTGGATTAAGGAAGAAACAATCTCTGATTGTACAGATTCTGCCGTCTCA 2065
QY 2533 TGACCAAAATTCGCAAGGAGTGCAGAGGTCTTGGCCCTTGAGGACTTCCAAACGGCCAAAC 2592
DB 2066 TGACCGAATTCGCAAGATGTGAATCTCTTGGCCCTTGAGGACTTCCGACTTCAGAAC 2125
QY 2593 GGTCTCACTGGCATGGTGCATCAGCTGGGAAGCCTGATTGGTCTGAGAAATAGCCGATTGG 2652
DB 2126 GGTGAAATGGCAGCGTGCATCAGCCCGGGAAGCCTGACTGGTCTAGAGGCAAGCCGATTGG 2185
QY 2653 TTGCCCTTTCCATGAAGATGAAAGACAGAGGCGGAGATCTATGTGGCCCTTCAACACCGACC 2712
DB 2186 TTGCCCTTCAACATGAAGACGAAACCAAGGCGAGATCTACGTGGCCCTTCAACACCGAGTC 2245
QY 2713 ACTTACCGCGCTGTTGAGCTCCAGAGCGCGCAGGCGCGGTGGGAACCGGTGGTGG 2772
DB 2246 ACCTTCCGCGTGGTGTGGGCTTCCAGAGCGCTCTGGGTTCGATGGAGCGCGGTGGTGG 2305
QY 2773 ACACAGGAAGCAGCAGCATTACGACTTCCCTCACCGACGACTTACCTGATCGCGCTCTCA 2832
DB 2306 ACACCGGCAAGAGGACCATATGACTTCTCACGATGGCTGCCAGATCGTGTCTCA 2365
QY 2833 CAATACACAGTTCTGCAATTTCTTACTCAACCTCTACCCCATGCTCAGTACTCAT 2892
DB 2366 CCGTCTACAGTTCTCTCATTTCTCACTCAATCTCTATCTCTATCTCTATGCTCAGCTACTCCT 2425
QY 2893 CGGTCACTCTAGTATGCGCCCTGATGTTTGAGAGACCAATATATA 2938
DB 2426 CAATCATCTCTGATTGGCCCTGATGCTGAAAAGAGCAGATACA 2471

RESULT 4
AAD47816
ID AAD47816 standard; cDNA; 2712 BP.
XX
AC AAD47816;
XX
DT 24-FEB-2003 (first entry)
XX
DE Alternative version of maize sugary1 (SUI) cDNA.
XX
KW Maize; starch debranching enzyme; sugary1; industrial application; SUI;
KW starch processing industry; gene; ss.
OS Zea mays.
FH Key
FT CDS
FT 1..2457
FT /tag= a
FT /product= "Alternative version of SUI protein #1"
FT /note= "No start codon"
FT /partial
XX
PN US6410716-B1.
XX
PD 25-JUN-2002.
XX
PF 24-FEB-1999; 99US-00256741.
XX

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PR 24-MAR-1995; 95US-00410784.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Myers AM, James MG;
XX WPI; 2002-616514/66.
XX P-PSDB; AAE29892.
XX
XX Novel starch debranching enzyme protein sugary1 or its polypeptide
XX fragment useful as replacement for bacterial and fungal enzymes currently
XX used in starch processing industry.
XX
XX Disclosure; Fig 1; 75pp; English.
XX
XX The invention relates to maize starch debranching enzyme, sugary1 (SU1)
XX and nucleic acid molecules encoding such proteins. SU1 sequences are used
XX as a replacement for the bacterial and fungal enzymes currently used in
XX the starch processing industry and as immunogens to raise antibodies
XX against SU1. Polynucleotides of the invention are useful as markers for
XX identification of specific corn varieties, for the development of corn
XX varieties with starch properties tailored for specific industrial
XX applications. The present sequence is an alternative version of maize SU1
XX cDNA. Note: This sequence is stated to be the same as that shown as SEQ
XX ID NO:1 (AAD42890) in column 31-38 of the specification. However the
XX sequences differ
SQ Sequence 2712 BP; 637 A; 644 C; 745 G; 686 T; 0 U; 0 Other;

Query Match 33.4%; Score 1000; DB 6; Length 2712;
Best Local Similarity 65.7%; Pred. No. 9e-206;
Matches 1883; Conservative 0; Mismatches 350; Indels 633; Gaps 4;

Qy 79 CGGTGTCGAGCGCGGACGAAGAGTAGAGGACGAGGGGAGGAGGAGCGCGGTGCGG 138
Db 233 CCGTGGCGAGCGGTGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 292
Qy 139 AGGACAGGTAGCGCTCGCGCGCGCGGTGCGAGGAGGAGGAGGAGGAGGAGGAGG 198
Db 293 AGGAGAGGTTGCGCTCGCGCGCGCGGTGCGAGGAGGAGGAGGAGGAGGAGGAGG 352
Qy 199 GCGCCACCGCGCTCGCGCGCGCGGTCAATTTGCGCGGTCTATTCGCGGGAGGAGG 258
Db 353 GCGCCACCGCGCTCGCGCGCGCGGTCAATTTGCGCGGTCTATTCGCGGGAGGAGG 412
Qy 259 CGCGCTCTGCTCTTCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 318
Db 413 CGTGGCTGAGGCTCTTGGCTCGCGCGCGCGGTCAATTTGCGCGGTCTATTCGCGGG 449
Qy 319 GTTCATCAGCTTTGCGTGGCGCGCGCGGTCTATTTGCGCGGTCTATTTGCGCGGT 378
Db 450 ----- 449
Qy 379 CTGGGCAAAATGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 438
Db 450 -----GGATAGGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 492
Qy 439 CGGACCGGAAACGTGCGAGTGTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 495
Db 493 CGAACCGGAAACGTGCGAGTGTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
Qy 496 GGGTACAGGTTGCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555
Db 553 GGATACAGGTTGCGAGTGTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
Qy 556 GTCTGTGTGATCTTATGCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 615
Db 613 GTTGTGTGTGATCTTATGCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
Qy 616 CGTGGTAAACATTTGCTGGCTCAGATGGCTGGATGATCCCTCTTCCATATAGCAGTTT 675
Db 673 CCTGGTGGTGTGTTGGCTCAAAATGGCTGGATGATCCCTCTTCCATATAGTATTT 732

Qy 676 GATTGGGAAGGCGACCTACCTAAGATATCTCTCAAAAGGACCTCGTATATATGAGATG 735
Db 733 GATTGGCAAGGTGACCTTACCTTGGGTACCAATCAAGAGGACCTTGTATATATGAATG 792
Qy 736 CACTTGCCTGGATTCAAGAACATGTTCAAGCAATGTAGAACATCCCGGTACTTTTCAAT 795
Db 793 CATTTGCGTGGATTCAAAAGCACAATCAAGCAAGACAAAACACCCAGGAACCTTACAT 852
Qy 796 GGAGCTGTGCGAAGCTTGAAGCTTGAAGGAGCTTGAAGGAGCTTGAAGTATGAAATTAATG 855
Db 853 GGTGTGTGTCAAGCTTGAAGCTTGAAGGAGCTTGAAGGAGCTTGAAGTATGAGGATATG 912
Qy 856 CCCTGCCATGAGTTCAAGGAGCTGGAGTACTCAACCTCTTCTTCCCAAGATGAACCTTTGG 915
Db 913 CCCTGCCATGAGTTCAAGGAGCTGGAGTACTCAACCTCTTCTTCCCAAGATGAACCTTTGG 972
Qy 916 GGAATTTCTACCAATAACTCTTTTCAACCAATGACAGATACACATCAGCGGGGATATAA 975
Db 973 GGAATTTCTACCAATAACTCTTTTCAACCAATGACAGATATTTCTTCAAGTGGCATAGA 1032
Qy 976 AACTGTGGCGGTGATGCCATMAATGAGTTCAAAAGCTTTTGAAGAGAGGCTCACAAACGG 1035
Db 1033 GACTCTGGATGTGGTGGCCATAAATGAATTTAAAGCTTTTGAAGGAGGAGGAGGAGG 1092
Qy 1036 GGAATGTAGGTGATCCTGGATGTTCTTCAACCATACAGCTGAGGGTAAATGAGAAATGGT 1095
Db 1093 GGAATGTAGGTGATCCTGGATGTTCTTCAATCATACAGCTGAAAGGTAATGAGAAAGGC 1152
Qy 1096 CCAATATTATCATTTAAAGGGGTGCGATATACTACATCATATATCTTCTGACCCAAAGGA 1155
Db 1153 CCAATATTATCTTTTGAAGGGATAGATAATAGTACTACTACATCTTCTGACCTTAAGGA 1212
Qy 1156 GAGTTTATAAATTTCTTGGTGTGGGAATACCTTCAACTGTATCATCTCTGTGTGTTGCT 1215
Db 1213 GAGTTTATAAATTTCTTGGTGTGGGAATACCTTCAACTGTATCATCTCTGTGTGTTGCT 1272
Qy 1216 CAATTCNTGTAGATGTTTAAAGTACTTGGGTGACGGAATGCATGTTGATGTTTGTGTT 1275
Db 1273 GAATTTATAGTGGATGTTGATGATCTGGGTAAACAGAAATGCATGTTGATGTTTGTGTT 1332
Qy 1276 TTTGATCTTGATCCATATGACAGAGGTTCCAGTCTGTGGATCCAGTTTAAACGTGTAT 1335
Db 1333 TTTGACCTTGATCTATATCTGACAGAGGATGACGCTATGGGATCCAGTTTAAATGTAT 1392
Qy 1336 GAGCTCCAAATAGAAGGTGACATGATCAACAGGAGACCTCTTGTGTTACTCCACACATTT 1395
Db 1393 GGAAGTCCAATGGAAGGTGACATGATCAACAGGAGACCTCTTGTGTTGCTCCACACATTT 1452
Qy 1396 ATTGACATGATCAGCAATGACCCCAATTTCTTGGAGCGGTCAAGCTCATTTGCTGAAGCATGG 1455
Db 1453 ATTGACATGATGCAATGACCCCAATTTCTTGGAAATGTCAAGCTCATTTGCTGAAGCATGG 1512
Qy 1456 GATCAGGAGGCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGTGG 1515
Db 1513 GATCAGGAGGCTCTCTATCAAGAGGTGAGTTTCTCTCACTGGAAGCTTTGGTCAAGTGG 1572
Qy 1516 AATGGAGTACCGGACATTTGCGGTCAATTTCAATTAAGGACATGAGTGGTCTGCTGGT 1575
Db 1573 AATGGAAAGTACCGGACATCCCGTGGTCAATTTCAATTAAGGACATGAGTGGTCTGCTGGT 1632
Qy 1576 GGTTTTGGCAATGTCTTTGTGGAAGTCCACACCTATATACAGGTAAAGTTTGTGGCAATACT 1635
Db 1633 GCTTTTGTGCAATGTCTTTGTGGAAGTCCACAGTTTATAC----- 1671
Qy 1636 TGTAATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCATGATGATACACA 1695
Db 1672 ----- 1671
Qy 1696 TCTAAATATAAACAATCATAGTGTATGATGATGATGCTTGGCTAAGAGATATTAGTGTAT 1755
Db 1672 ----- 1671
Qy 1756 ACAGTAGTCTATATATAGTTTAAACACCCCAACTTGCAATGAAGGAACATATAGGCTTTT 1815

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Db 1672 ----- 1671
Qy 1816 CTAGTTATCTTATTATTGTCGGTGAATAATCCACTGAAATAATCCAGCCATGTCAAT 1875
Db 1672 ----- 1671
Qy 1876 TTTTAGGGGGGAGAGAACTATATTGATTGTCGCCCTAAAGAGCCATCTCAGAAAT 1935
Db 1672 ----- 1671
Qy 1936 TCATAGGTAACTTGTCTTCTGTAAAGAAAGAAAGCACTTTCATCTTTCTATCGGTGC 1995
Db 1672 ----- 1671
Qy 1996 TAACTTAGTCGATGATATATTGTAAGATGAATGCCAAATTAATTGTCGGATAATTG 2055
Db 1672 ----- 1671
Qy 2056 ATCTGTTATTCAAAATTTCTATTGTTGTTCTCTAGAAATCAAAACAGTAACCTGTTATT 2115
Db 1672 ----- 1671
Qy 2116 GGCCTGCAACTTCTTATTGATTAATCAGGAGAGAGAAACCTTGGCACAAGTATCA 2175
Db 1672 ----- 1705
Qy 2176 ACTTTGATGTGACATGATGATTTACCTGCTGATTTGGTAAACATATAATAAAGAT 2235
Db 1706 GCTTTGATGTGACATGATGATTTACCTGCTGATTTGGTAAACATATAATAAAGAT 1765
Qy 2236 ACAATTTACCAATTTGGGAGAACACAGAGATGAGAGAAATCAATCTTAGCTGGAAT 2295
Db 1766 ACAATTTGTCAAATGGTGAGACTTCAGAGATGGGAAATCATATCTTAGCTGGAAT 1825
Qy 2296 GTGGGAGGAGAGAAATTCAGAGATGCTGTCAAAGATTTGAGGAGAGGACATGC 2355
Db 1826 GTGGGAGGAGGAGAAATTTGCAAGTCTGTCAGTCCGAGATTAAGGAGAGGCAATGC 1885
Qy 2356 GCAATTTCTTTGTTGCTCATGTTTCTCAAGAGATTCCTCAATGTTCTACATGGGTGATG 2415
Db 1886 GCAATTTCTTTGTTGTTGTTGTTGTTCTCAGGAGTTCCATGTTCTACATGGGTGATG 1945
Qy 2416 AATATGGCCACAAAAAGGGGGCAACAAATACATACATCTGCTGATGTTTATGTCAAT 2475
Db 1946 AATATGTTCAACAAGGGGAGGAAACAAATACATACATCTGCTGATGTTTATGTCAAT 2005
Qy 2476 ATTTTCGCTGGATAAAA---AAGAACAACTCTGAGTTGCAACCGATTCGTGCTCA 2532
Db 2006 ATTTCCGTTGGATTAAGAGGAGAAACAAATCTCTGATTTGTACAGATTCGCGTCTCA 2065
Qy 2532 TGACCAATTCGCAAGAGTGCAGGTTCTTGCCCTTGAGGACTTTTCCAAAGGCCAAAC 2592
Db 2066 TGACCGAATTCGCAAGAGTGTGAATCTCTTGCCCTTGAGGACTTCCGACTTCAGAAC 2125
Qy 2592 GGCTGCAATGCGATGCTCATGAGCTGGAGCTGATGCTGCTGAGATAGCCGATTCG 2652
Db 2126 GGTGAAATGCGACGGTTCATAGCCCGGAGCTGACTGCTGAGAGGCAAGCCGATTCG 2185
Qy 2652 TTGCTCTTTCCATGAAGATGAAGACAGGCGGAGATCTATGTGGCTTCAACACAGCC 2712
Db 2186 TTGCTCTTCAACATGAAGACGAAACCAAGAGAGATCTACGTGGCTTCAACACAGTC 2245
Qy 2712 ACTTACCGCGTGTGTTGAGTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2772
Db 2246 ACTTTCGCGTGTGTTGAGTCCAGAGCGCTTCCAGAGCGCTTGGGTTCCGATGGGCGG 2305
Qy 2772 ACACAGCAAGCCAGCAGCAGCAGTCTCTCAGCAGCAGCAGTCTTACCTGATCGGCTCTCA 2832
Db 2306 ACACCGCAAGGAGGACCATATGACTTCTCAGCGATGGCTTCCAGATCTGTTGCTCA 2365
Qy 2832 CCATACACAGTTCCTCGATTTCTCTATCTCTCAACTCTTACCCCATGCTCAGTACTCAT 2892
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Db 2366 CGTCTACAGTTCTCTCATTTCTCAACTCTCTATCTATCTATCTATCTATCTATCTCT 2425
Qy 2893 CGGTCACTCTAGTATTGGCCCTGATGTTTGAGAGACCAATATATA 2938
Db 2426 CCATCATCTTGTATTGGCCCTGATGTTCTGAAAGAGCAGATACA 2471

RESULT 5
AD AAD42890 standard; cDNA; 2715 BP.
XX AC AAD42890;
XX 24-FEB-2003 (first entry)
XX DE Maize sugary1 (SUI) cDNA.
XX KW Maize; starch debranching enzyme; sugary1; industrial application; SUI;
XX OS Zea mays.
XX FT Key Location/Qualifiers
XX CDS 88..2454
XX FT /*tag= a
XX FT /product= "SUI protein"
XX FT /note= "No stop codon"
XX FT /partial
XX PN US6410716-B1.
XX PD 25-JUN-2002.
XX PF 24-FEB-1999; 99US-00256741.
XX PR 24-MAR-1995; 95US-00410794.
XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX PI Myers AM, James MG;
XX WPI: 2002-616514/66.
XX P-PSDB; AAE25588.
XX Novel starch debranching enzyme protein sugary1 or its polypeptide
XX fragment useful as replacement for bacterial and fungal enzymes currently
XX used in starch processing industry.
XX Claim 20; Col 31-38; 75pp; English.
XX The invention relates to maize starch debranching enzyme, sugary1 (SUI)
XX and nucleic acid molecules encoding such proteins. SUI sequences are used
XX as a replacement for the bacterial and fungal enzymes currently used in
XX the starch processing industry and as immunogens to raise antibodies
XX against SUI. Polynucleotides of the invention are useful as markers for
XX identification of specific corn varieties, for the development of corn
XX varieties with starch properties tailored for specific industrial
XX applications. The present sequence is maize SUI cDNA. Note: This sequence
XX is stated to be the same as that shown as SEQ ID NO:1 (AAD47816) in
XX figure 1 of the specification. However the sequences differ
XX
XX Sequence 2715 BP; 637 A; 645 C; 747 G; 686 T; 0 U; 0 Other;
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Query Match 33.0%; Score 989; DB 6; Length 2715;
Best Local Similarity 65.7%; Pred. No. 2.1e-203;
Matches 1883; Conservative 0; Mismatches 350; Indels 634; Gaps 5;
Qy 79 CGGTTGTCTGAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138
Db 235 CCGTGGCCGAGCGGTTGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 294
Qy 139 A-GGACAGTACGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 197
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QY 2355 CGCAATTTCTTTGTTGTTCTCATGTTTCTCAAGGAGTTTCCAAATGTTCTACATGGGTGAT 2414
 Db 1888 CGCAATTTCTTTGTTGTTCTTTATGTTTCTCAGGGAGTTTCCAATGTTCTACATGGGGCAT 1947
 QY 2415 GAATATGCGCCACACAAAGAGGGGCAACAATAATACATACACTGCCATGATTTCTTATGTCAAT 2474
 Db 1948 GAATATGGTACACAAAGGGAGGAGACACAAATACGTACTTGCATGACCAATATATGTCAAT 2007
 QY 2475 TATTTCCTCGTGGATATAAAA---AGAAACAATATCTCTGAGTTGACCCGATTTCTGTGCTTC 2531
 Db 2008 TATTTCCTCGTGGATATAAGAGAGAGAAACAATCTCTGATTTGACAGATTTCTGCGCTCTC 2067
 QY 2532 ATGACCAAAATTCGCAAGGAGTGGAGGGTCTTGCGCTTTCAGGACTTTTCCAAAGGGCAAA 2591
 Db 2068 ATGACCGAATTCGCAAGAGATGTAATCTCTTGCGCTTTCAGGACTTTCCGATTCAGAA 2127
 QY 2592 CGGCTGACGTGGCATGTTGATTCAGCCTGGGAAGCCTGATTTGGTCTGAGAAATAGCCGATTC 2651
 Db 2128 CGGTTGAATGGCACGGGTCTATCAGCCCGGAAGCCTGACTGGTCAGAGGCAAGCCGATTC 2187
 QY 2652 GTTGCCTTTTCCATGAAGATGAAGACAGGGGAGATCTATGTGGCTTTCACACACAGC 2711
 Db 2188 GTTGCCTTTTCCATGAAGAGGAGAAACCAAGGGGAGATCTATGTGGCTTTCACACACAGT 2247
 QY 2712 CACTTACCGGCGGTGTTGTTGAGCTCCACAGAGCGCGCGGCGCGGTGGGAACCGGTGGTG 2771
 Db 2248 CACCTTCGGTGGTGTGTTGGGCTTCCAGAGCGCTCTGGTTCGATGGAGCGGTGGTG 2307
 QY 2772 GACACAGGCAAGCCAGACACATAGACTTCTCTACCGAGACTTACCTGATCGGCTCTC 2831
 Db 2308 GACACCGGCAAGGAGGACCATATGACTTCTCTACCGATGGCGCTGCCAGATCGTGTGTC 2367
 QY 2832 ACCATACACAGTTCCTCGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2891
 Db 2368 ACCGTCTACAGTTCCT 2427
 QY 2892 TCGGTCTATCTCTGATTTGCGCCCTGATGTTTGGAGACCAATATATA 2938
 Db 2428 TCCATCATCTCTGATTTGCGCCCTGATGTTGAAAGAGCAGATACA 2474

RESULT 6

AAAX27061

ID AAX27061 standard; DNA; 2706 BP.

XX AC AAX27061;

XX 21-MAY-1999 (first entry)

XX S. tuberosum isoamylase clone 15 coding sequence.

DE Isoamylase clone; potato; branched polysaccharide synthesis; amylopectin;
 KW starch modification; debranching activity; ss.
 KW

XX Solanum tuberosum.

XX WO9906575-A1.

XX 11-FEB-1999.

XX 30-JUL-1998; 98WO-GB002280.

XX 31-JUL-1997; 97GB-00016185.

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX Edwards EA, Smith AM, Martin CR, Bustos Guillen R;

XX WPI; 1999-153803/13.

XX P-PSDB; AAY00869.

XX New nucleic acid from potato encoding starch debranching enzyme with

XX isoamylase activity - and related vectors, transformed cells and plants.

PT proteins and antibodies, used to generate starch with altered properties,
 PT for use in foods, as thickeners etc.
 XX Claim 3; Fig 2; 78pp: English.

XX This sequence encodes a Solanum tuberosum isoamylase of the invention.
 CC Fragments of the isoamylase coding sequence are used to identify and
 CC clone isoamylases from other plant species, by standard hybridisation or
 CC amplification methods. Expression of the isoamylase DNA in host cells is
 CC used to produce the isoamylase which is used: (i) to raise antibodies
 CC (Ab) for identification, isolation and localisation of isoamylases; and
 CC (ii) for synthesis of branched polysaccharides. The DNA, proteins and Ab
 CC (or related peptides) are used to alter the quality and quantity of
 CC polysaccharides in a host cells, specifically to alter branching in
 CC amylopectin. The modified starches produced are useful in human or animal
 CC foods; as biodegradable plastic; as food or paint thickener; in starch-
 CC coated films, paper and textiles; in mining explosives; in
 CC pharmaceuticals and glues. Manipulation of debranching activity in a
 CC plant allows control of starch properties, e.g. increased gel strength;
 CC formation of paste rather than gel, changed physical characteristics etc
 XX Sequence 2706 BP; 797 A; 492 C; 524 G; 792 T; 0 U; 1 Other;

Query Match 22.5%; Score 673.2; DB 2; Length 2706;

Best Local Similarity 69.4%; Pred. No. 3.4e-135;

Matches 937; Conservative 0; Mismatches 398; Indels 15; Gaps 1;

QY 395 AGGATAGGTGTCACGAGGAGGTCCCTTGACCCCTGATCAATCGGACCGGACGCTGT 454

Db 425 AGAAGAGAGTACCGAGCAAAATTTCTGGATCTCTAGCTAATAAACTGGAGATGAT 484

QY 455 GGCATGTCTTCATCGAAGCGAGGTGCACAAATGTTTACGGGTACAGGTTTCGACGGCA 514

Db 485 GGCATGTGTCTTAAGGAGATTTTGAGATATGCTATATGGTACAAATTCGATGGGA 544

QY 515 CTTTTGCTCTCACTGCGGGCACTACTTGTATGTTTCCATGTCGTGGTGTGATCTTATG 574

Db 545 AATTCGTCTTGAAGAAGGACACTACTTGTGACTCTTCGAGATAGTGTGTGATCTTATG 604

QY 575 CTAGGCGAGTGTAAAGCGGAGGATGTTGTTTCCAGCGCGTGTAAACAATTCGCTGGC 634

Db 605 CCAGGCTATAGTAAGCAGAGGAGATATGTTGTTATAGGCCAGAGATGATTTGTTGGC 664

QY 635 CTCAGATGGCTGGCATGATCCCTCTTCCATATAGACAGCTTTTGTATGGGAAGCGACCTAC 694

Db 665 CCCCAATGGCTGGCATGTTGTTGCTTCTGCTTCTGATCATGTTTGTGGGAAGGAGATCTAC 724

QY 695 CTCCTAAGATATCTCCAAAGGACCTGTTAATATATAGATGCATTTGCTGCTGATTCACGA 754

Db 725 CACTGAAGTTTCCACAGAGAGATCTTGTATCTATGAATGATGTTGCTGGGTTTACTA 784

QY 755 AGCATGATTCGAAGCAATAGAACATCCGGTACTTTTCATTTGGAGCTGTGTGCAAGCTTG 814

Db 785 ATCATGAGTCGAGTGAACAAAATATCTCGTACTTACCTTGGTGTGTTGTGAGAACTTG 844

QY 815 ACTATTGAAGAGGTTGGAGTTAATGTTATTAATTAATGCTCCCTGCGCATGATTCACAG 874

Db 845 ATCACTTGAAGGAACTTGGTGTCAACTGTATAGAGCTAATGCCCTGTCCAGAGTTCAATG 904

QY 875 AGCTGGAGTACTCAACCTCTTCTTC-CAAGATGAACCTTTTGGGAT 919

Db 905 AGCTGGAGTACTATAGTTATAACTCTGTATTGGCGACTACAAGTTTAACTTTTGGGCT 964

QY 920 ATTCTACCATAACTTCTTTTCCCAATGACAGATACATCAGGCGGGAATAAAACT 979

Db 965 ATTCTACTGTCAATTTCTTTTCCCAATGGGAAGATCTCATCTGCTGGTCTAAGTAAT 1024

QY 980 GTGGCGGTGATGCCAATAAATGAGTTCAAAACTTTTGAAGAGAGGCTCACAAACGGGAA 1039

Db 1025 GCGGCTCGGTGCAATAAACGAATTTAAGTATCTTGTCAAGAGAGACATAAACGTGAA 1084

QY 1040 TTGAGGTGATCTGATCTTCTTCAACCATATAGCTGAGGGTAATGAGTAATGGTCCA 1099

Db 1085 TCGAGGTTATCATGGATGTTGTTTCAATCACAAGGCTGCTGAAGAAATGAAATGGTCCCA 1144
Qy 1100 TATTATCAATTAAGGGGTGCAATAACTACTATATATATGCTTGCACCAAGGAGAGT 1159
Db 1145 TACTATCATTTAGAGGCAATGACACAGTGTGTTTATACGCTAGCTCTTAAGGTTGAAT 1204
Qy 1160 TTTATRACTATCTGGCTGTGGGATGACCTCAACTGTAATCATCTGTGTTGTCFCAAT 1219
Db 1205 TTTACAACACTACTAGGATGTGGAAATACCTTCAACTGTAATATCCATTTGTAACGTCAT 1264
Qy 1220 TCATTGTAGATTGTTTAAAGTACTGGGTGACGGAATGCAATGTGTGTTGTTTTCGTTTGG 1279
Db 1265 TTAATAGTGGATTGCTTCAGATATTGGGTACCGAAATGCAAGTAGATGGCTTCGCTTGG 1324
Qy 1280 ATCTTCATCCATTAATACACAGAGGTTCAGTCTGTGGATCCAGTTAAGCTGTATGGAG 1339
Db 1325 ATCTTGTCTTATCTTACAAAGATGACAGCTCGTGGATGCTGTAATGTCTATATGGAA 1384
Qy 1340 CTCNAATAGAGGTGACATGATCACAACAGGGGACACCTCTGTGTACTCCACCACTTATTG 1399
Db 1385 ATTCAATTGACGGTGAAGTATCACCACAGGCACCTCTCTCAAGCCCACTTGTATTG 1444
Qy 1400 ACATGATCAGATGACCCCAATCTTGGAGGGGTCAAGCTCATGTGTGAAGCATGGGATG 1459
Db 1445 ATATGATTAGCAATGATCCCAATCTTCGTGGAGTAAAGCTTATAGCTGAAGCATGGGATT 1504
Qy 1460 CAGGAGCCCTATCAAGTAGGTCAATTCCTCACTGGATGTTTGTCTCTGAGTGGAAATG 1519
Db 1505 GTGAGGCCCCATTACCAAGTTGGCATGTTCCGCACCTGGGTATCTGTGCGAGTGGAAAG 1564
Qy 1520 GGAAGTACCGGACATGTCGTCATTTCAATTAAGGCACTGATGATTTGCTGTGGTTT 1579
Db 1565 GAAAGTACCGTGAATGTCAGGCGAGTTTCATCAAGGCACTGATGGTTTTCGTGGGCTT 1624
Qy 1580 TTGCGGATGCTTTTGGAGTCCACCTATACAGGTAAGTTGTGGCAATCTTGTAT 1639
Db 1625 TTGCTGAATGCTTTTGGAGGCCAAATCTATACCAAGAGGAGGAGGAGGAGG 1684
Qy 1640 AATGAGTTGATGTAATGTCACCTGGATTTTATATATATACCATGATGATACACATCTA 1699
Db 1685 ACAGTATAATTTGCTGTGTCACCATGTTTACTTTGGCTGATTAGTGACATACA 1744
Qy 1700 AATATATAACAATCATAGTATGATGATG 1729
Db 1745 ACRATAACAATTTGGCAATGGAGAGG 1774

RESULT 7

ABZ12413

ID ABZ12413 standard; DNA; 2352 BP.

AC ABZ12413;

XX 21-JAN-2003 (first entry)

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 219.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX WO200216555-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-024647P.

XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

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XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 218; 577pp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX in methods of the invention. Note: The sequence data for this patent is
XX not represented in the printed specification but is based on sequence
XX information supplied to Derwent by the European Patent Office
XX Sequence 2352 BP; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;
XX

Query Match 22.0%; Score 658.4; DB 6; Length 2352;

Best Local Similarity 71.2%; Pred. No. 5e-132;

Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

Qy 389 TGCTCAGATAGGTTGACCGAGGAGTTCCCTTGACCCCTGATGATCGGACCGGA 448
Db 323 TCCGTGAGCAAAAGTACCGGAGGAGATTCAGCTTGATCCATCAAGGAATAGACTGCC 382

Qy 449 AGCTGTGCATGCTCTTCATCGAAGCGAGTGCACAACATGTTTACGGGTACAGTTGCG 508
Db 383 ATGTTTGGCATGTTCTTGAGAGAGATTTCAAGATATGTTGATGTTATAGATTG 442

Qy 509 ACGGACCTTTGCTCCTCACTGCGGGCACTACCTTGATGTTTCCAAATGCTGCTGGATC 568
Db 443 ATGGCAAGTTTCTCCTGAAGAAGTCTATTATGATTTCTCCAACTTTATTGGATC 502

Qy 569 CTATGCTAAGCAGTATAGCCAGGAGTATGGTTTCCAGCGCTGTAACAATT 628
Db 503 CTACGCAAGGCAATTAAGCAGAGATGAGTTTGGAGTTTGGGACTGATGATAAT 562

Qy 629 GCTGCGCTCAGATGGCTGGCATGATCCCTCTTCCATATAGCAGCTTTTGAITGGGAAGCG 688
Db 563 GTTGGCTCAATGCGGTGATGGTACCCTCGTGAAGAGATTTCATTGGGAAGGG 622

Qy 689 ACCTACCTCTAAGATATCCTCAAGGACCTGGTAAATATATGAGATGACATTCGCTGGAT 748
Db 623 ATATGCATCTGAAGCTTCCACAGAAAGATCTTGTATATATGAAATGATGTCGAGGTT 682

Qy 749 TCACGAAGCATGATTCAAGCAATGAGAACATCGGGTACTTTCATTGAGCTGTGTCGA 808
Db 683 TTCAAGGATGAGTCTAGTAAATGAAATTTCCCTGGCAGATACAGGGTGTTCAGAGA 742

Qy 809 AGCTTGACTATTGGAAGGAGCTTGGAGTTAATTTGTTAATTAATGATCCCTGCCATGAGT 868
Db 743 AGCTTGACCATTTGAAGGAGCTTGGGATAAATTTGATAGAATTAATGCAATGTCACGAGT 802

Qy 869 TCAAGAGCTGGAGTACTCAACCTTCTCTTC-----CAAGATGACTTTT 913
Db 803 TTAATGAGCTGGAGTATTACAGCTACAATGATTTTGGGAGACCCACAGGGTAAATTTT 862

Qy 914 GGGGATATTTACCATAAACTTTCTTTTCCCAATGACAAGATACATCAGCGGGGATAA 973
Db 863 GGGGTTACTCTACCATTTGGTTCTTCTCGCCATGATCAGATACGATCAGCAAGCTCTA 922

Qy 974 AAAACTGTGGGCGTATGCCATAAATGAGTTCAAACTTTTGTAGAGAGCTCACAAC 1033
Db 923 ACAATTTTGTGGACGAGCCATAAATGAATTCAAAATTTCTTGTTAAGGAGGCACATAAC 982

QY 1034 GGGGAATTGAGGTGATCTCTGATTTGTTCTTCAACCATACAGCTGAGGGTAATGAGAATG 1093
 XX |||||
 PS |||||
 DB 983 GAGGAATTGAGTAAATCATGATGCTGCTTTGAACACACAGCGGAAGGAATGAAAAG 1042
 CC |||||
 CC 1094 GTCCAAATATATCAATTAAGGGGTGATATATCACTATATATGCTTGGACCCCAAGG 1153
 CC |||||
 CC 1043 GGCCCAATTTCTCAATTTAGAGGAGTTGATAACAGTGTCTATTACATGCTTGTCTCCAAAGG 1102
 CC |||||
 CC 1154 GAGAGTTTATAACTATTCTGGCTGTGGGAATACCTTCAACTGTATATCATCTCTGGGTTT 1213
 CC |||||
 CC 1103 GCGAGTCTATAATATTAGGCTGTGGTAATCAATTCATCACTGCAATCATCTGTGGTGC 1162
 CC |||||
 CC 1214 GTCAATTCATTTAGATGTTTAAAGTACTGGGTGACGGAATATGCAATGTTGATGTTTTC 1273
 CC |||||
 CC 1163 GTCAATTCATATTGGATTGCTGAGATATTGGGTTACAGAAATGCAATGTTGACGGCTTC 1222
 CC |||||
 CC 1274 GTTTTGATCTTGCATCAATATGACACAGAGTTCCAGTCTGTGGATCCAGTTAAAGTGT 1333
 CC |||||
 CC 1223 GCTTTGATCTTGTTCATCAATGTCAGGAGCAGCCCTTGGGATGAGCCCAATGTTT 1282
 CC |||||
 CC 1334 ATGAGCTCCCAATAGAAGGTGACATGATCAACAGGGACACCTCTTGTCTTACTCCACAC 1393
 CC |||||
 CC 1283 ACGGGCTGATGTAGAAGGTGACTTGTCTCAACTGGTACTCTTAATAGCTGCCCTCCAG 1342
 CC |||||
 CC 1394 TTATTGACATGATCAGCAATGACCCCAATTTCTGGAGCGTCAAGCTCATTTGCTGAGCAT 1453
 CC |||||
 CC 1343 TAAATTGACATGAATGAATGATCCAACTATCCGCGGTGTTAAGCTAATAGCTGAAGCAT 1402
 CC |||||
 CC 1454 GGGATGAGGAGGCTCTATCAAGTAGGTCAATTTCCCTCACTGGAATGTTTGTCTGAGT 1513
 CC |||||
 CC 1403 GGGATGCGGTGGCTGTACCAAGTTGGCATGTTCCACACTGGGTATTTGGTCTGAGT 1462
 CC |||||
 CC 1514 GGAATGGAGTACCGGCAATTTGTGCTCAATTCATTAAGGCACTGATGATTTGCTG 1573
 CC |||||
 CC 1463 GGAATGGAAGTTTCGGGATGTTGTGAGACAGTTTCATAAAGGACCGGATGGCTTTCTG 1522
 CC |||||
 CC 1574 GTGGTTTGGCGAATGCTTTGTGGAGTCCACACTATACCAAGTAAAGTTG 1625
 CC |||||
 CC 1523 GTGCTTTGCTGATGCTCTGTGGAGCCCAATCTGTACCAAGGAGGTAG 1574
 CC |||||

RESULT 8
 ADA67900
 ID ADA67900 standard; DNA; 2352 BP.

XX AC ADA67900;

XX XX 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 141.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX XX Arabidopsis thaliana.

OS WO2003000898-A1.

XX PN 03-JAN-2003.

XX XX 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant

PT gene expression.
 XX PS Claim 6; SEQ ID NO 141; 899pp; English.
 XX CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX SQ Sequence 2352 BP; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;

Query Match 22.0%; Score 658.4; DB 7; Length 2352;
 Best Local Similarity 71.2%; Pred. No. 5e-132;
 Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

QY 389 TGCTGCAGATAGGTGACCGAGAGGTTCCTTACCCCTGATGAATCGGACCGGA 448
 DB 323 TCCGTCAACAAGGTGACCGAGAGATTTCAGCTTGATCCATCAAGGAATAGAACTGCC 382
 QY 449 ACGTGTGCAATGCTTCATCGAAGCGAGCTGCACAATGCTTTACGGGTACAGGTTCC 508
 DB 383 ATGTTGGCATGTTCTTGTAGAGGAGATTTCAAAGATATGTTGTATGGTTATAGATTG 442
 QY 509 ACGGCACCTTTGCTCCTCACTGCGGCACTACCTTGATGTTTCCAATGTCGTGTGGATC 568
 DB 443 ATGCAAGTTTCTCCTGAAGAGGTCAATATATGATTCCTCCCAATTTATTTGATC 502
 QY 569 CTTATGTAAGCGAGTATAGAGCGAGGAGTATGTTGTTCCAGCGGTGTTAACTTT 628
 DB 503 CTTACCAAGGCAATATAGCAGAGATGAGTTTGGAGTTTGGGACCTGATGATTAAT 562
 QY 629 GCTGCGCTCAGATGCTGGCATGATCCTCTTCCATATAGCACGTTTGTGTTGGAAGCG 688
 DB 563 GTTGGCTCAAAATGGCTGATGTTATCCACTCTGTAGGAGAGTTTGTGTTGGAAGGG 622
 QY 689 ACCTACCTCTAAGATATCTTCAAAAGGACCTGTTAATATATGATGCATCCCTGCGT 748
 DB 623 ATATGCATCTGAAGCTTCCACAGAAAGATCTTGTATATATGAAATGCATGTGCGAGTT 682
 QY 749 TCAGAGCATGATCAAGCAATGTAGACATCCGGGTACTTTTCATTTGGAGCTGTGCGA 808
 DB 683 TTCAAGGCATGAGTCTAGTAAATTTGAATTCCTGCGCACATACAGGGTGTTCAGAGA 742
 QY 809 AGCTTGACTATTGAAGGAGCTTGGAGTTAATTTGATTTGAATTAATGCCCTGCCATGAT 868
 DB 743 AGCTTGACCAATTTGAGGAGCTTGGGATAAATTTGATAGAATTAATGCCATGTCAAGT 802
 QY 869 TCAAGAGCTGAGTACTCAACCTCTCTTC-----CAAGATGNACTTTT 913
 DB 803 TTAATGAGCTGGAGTATTACAGCTACAATACGATTTTGGGAGACCAAGGGTAAATTTT 862
 QY 914 GGGATATTCTPACCATAAACTTCTTTTCAACAATGACAAGATACATCAGGCGGGATAA 973
 DB 863 GGGGTACTCTACCATTTGGGTCTTCTGCGCCATGATCAGATAGCATCAGAGCTCTA 922
 QY 974 AAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTGAAGAGAGGCTCACAAC 1033
 DB 923 ACAATTTTGTGGAGCGAGCCATAAATGAATTTCAAATTTCTTTGAAGAGGCGCATTAAC 982
 QY 1034 GGGGAATTTGAGTGTATCTGATGCTGTCTTCAACCATACAGCTGAGGGTAATCAGAAATG 1093
 DB 983 GAGGAATTTGAGTAAATCATGATGCTCTTTGAACCAACACAGCGGAGGAATGAAGAAG 1042
 QY 1094 GTCCAAATATATCAATTTAAGGGGTGATTAATTAATCACTACTATGCTTTGACCCCAAGG 1153
 DB 1043 GGCCCAATTTCTCAATTTAGAGGAGTTGATAACAGTGTCTATTACATGCTTGTCTCCAAAGG 1102

Db 1268 GTGAATTTTCAACTACTCAGGATGTGGAATACCTTCAACTGTAATAATCCCAATTGTAC 1327
 Qy 1214 GTCAATTCATTTAGATTTTAAAGATACCTGGGTGACGGAAATGCAATGTTGATGGTTTTC 1273
 Db 1328 GTCAAT---TTATAGTATGCTGAGATATTGGGTACCGAAATGCGATACATGGCTTC 1384
 Qy 1274 GTTTTGATCTTCATATGACACAGAGTTCAGTCTGTGGATCCAGTTAAAGTGT 1333
 Db 1385 GCTTTGATCTTCTTCTATCTTACAAAGAAAGTAGCAGCTCGTGGAAATGCTGTAATGTCT 1444
 Qy 1334 ATGGAGCTCCAATAGAGGTGACATGATCAACAGGAGCACCTCTTGTCTTACTCCACCAC 1393
 Db 1445 ATGGAATTCNATGACGGTGACGTGATCACAGGCATCTCTCTCAAGCCCAACAT 1504
 Qy 1394 TTATTGATGATCAGCAATGACCAATTTCTGGAGCGTCAAGCTCATTTGCTGAAGCAT 1453
 Db 1505 TGATTGATATGATTAGCAATGATCCAAATCTTCTGGAGTAAAGCTTATAGCTGAAGCAT 1564
 Qy 1454 GGGATGACGAGGCGCTCTATCAAGTAGTCAATTCCTCACTGGAATGTTTGGTCTGAGT 1513
 Db 1565 GGGATTTGGAGGCGCTTTACCAAGTTGGCATGTTTCCGCACTGGGTATCTGTGCGAGT 1624
 Qy 1514 GGAATGGGAAGTACCGGACATTTGCGTCAATTCATTAAGGCGTCAAGCTCATTTGCTG 1573
 Db 1625 GGAACGGAAGTACCGTGACATGCTACGGCAGTTTCATCAAGGCATCTGATGGGTTTCTG 1684
 Qy 1574 GTGGTTTGGCAATGCTTTGGGAAGTCCACACCTATACCAAGTAAAGTTGTTGGCAATA 1633
 Db 1685 GGGCTTTTGGTGAATGCTTTGTGAAGCCCAATCTATACCAAGAGGAGGAAGAAAC 1744
 Qy 1634 CTCTGAATGAGTTGAGTGAATGTCACCTCGATTTTATATATATACCAATGATGATACA 1693
 Db 1745 CATGACAGATATAAATTTCTGTGTGTCGCCACAGTGTGTTTACTTTGGCTGATTTAGTGA 1804
 Qy 1694 CATCTAATATATAACAATCATAGTGTATGATG 1729
 Db 1805 CATACAACATAAACAATAATTTGGCAATGGAGAGG 1840

RESULT 10

AAT96754
 ID AAT96754 standard; cDNA to mRNA; 2133 BP.

AC AAT96754;

DT 25-MAR-2003 (revised)
 DT 08-MAY-1998 (first entry)

XX S. tuberosum debranching enzyme cDNA.

XX Debranching enzyme; PDB; potato; transgenic plant; starch; industry;
 KW food manufacture; ss.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FT CDS 1..1822

FT /*tag= a

FT /product= "debranching enzyme"

FT /note= "partial coding sequence"

XX DE19618125-A1.

XX 13-NOV-1997.

XX 06-MAY-1996; 96DE-01018125.

XX 06-MAY-1996; 96DE-01018125.

XX (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

XX WPI; 1997-551167/51.

DR P-PSDB; AAW36602.
 XX DNA encoding potato debranching enzyme - useful for producing recombinant
 PT enzyme or transgenic plants for use in food production or in industry.
 XX Claim 1; Page 14-17; 20pp; German.
 XX This cDNA sequence encodes a novel potato debranching enzyme (PDE). This
 CC gene can be used in the production of transgenic plants especially starch
 CC storing plants e.g. Cereal or potato plants. Other nucleic acid molecules
 CC could be designed which specifically hybridise to the PDE transcript and
 CC inhibit its translation. Vectors containing this gene can be linked in
 CC sense orientation with regulatory elements that ensure its transcription
 CC and translation in prokaryotic and eukaryotic cells. The starch produced
 CC from such transgenic plants could be used in the manufacture of foods or
 XX industrial products. (Updated on 25-MAR-2003 to correct PA field.)
 SQ Sequence 2133 BP; 650 A; 392 C; 475 G; 616 T; 0 U; 0 Other;

Query Match 19.2%; Score 575.4; DB 2; Length 2133;

Best Local Similarity 59.8%; Pred. No. 4.1e-114;

Matches 799; Conservative 0; Mismatches 331; Indels 15; Gaps 1;

Qy 600 GTATGTTTCCAGCGGTGTTAAACAATTGCTGCCCTCAGATGCTGGCATGATCCCTCT 659
 Db 1 GAAATTCGSCACGAGGGCCAGAGGATGATTGTTGGCCCCCAATGCGAGCGCATGGTACCTTC 60
 Qy 660 TCCATATAGCACGTTTGAATGGGAAGCGGACCTACTCTAAGATATCTCAARAGGACCT 719
 Db 61 TGCCTCTCATCAGTTTGAATGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGATCT 120
 Qy 720 GGTAAATATAGATGCACTTGCCTGGATTCCAGAACGATGATTCAGAACATGTAGAACA 779
 Db 121 TGTATCTATGAATGCATGTTCTGGATTACAAATCATGAGTCGAGTGAACAAAATA 180
 Qy 780 TCCGGTACTTTCAATTGGAGCTGTGCAAGCTTGACATTTTGAAGAGCTTGGAGTTAA 839
 Db 181 TCCTGGTACTTACCTTGGTGTGTGGAGAACTTGTATCCTTGAAGAACTTGGTGTCAA 240
 Qy 840 TTGTATTGAATTAATGCTCCCATGAGTTCAACAGCTGGAGTACTCAACCTCTTCTTC 899
 Db 241 CTGTATAGCTAATGCTCTGACGAGTTCAATGAGCTGGAGTACTATAGTTATATCTC 300
 Qy 900 -----CAAGATGAACCTTTTGGGGATTTCTACCAATAAATCTTTTTCACC 944
 Db 301 TGTATTGGGCGACTACAAGTTTAACTTTTGGGGCTATTCTACTGTCAATTTCTTTTCTCC 360
 Qy 945 AATGACAGATACACATCAGCGGGATATAAATACTGTGGGCGTGATGCCATAATGAGTT 1004
 Db 361 AATGGGAAGTACTCGTCTGCTGCTAAGTAAATGCGGCTCGTGCAATTAACGAAAT 420
 Qy 1005 CAAACCTTTTGAAGAGAGGCTCACAACCGGGGAATTCAGGTGATCTCGGATGTGTCTT 1064
 Db 421 TAAGTATCTTGTCAAGGAAGCACATAAACGTGGAATCGAGGTTATCATGATGTTGTTT 480
 Qy 1065 CAACCATACAGCTAGGGAATGAGATGTCCTCAATATTATCATTTTAAAGGGTTCGATA 1124
 Db 481 CAATCACACTCTGTAAGGAAATGAAATGGTCCCATATCATATTAGAGGCATTTGACAA 540
 Qy 1125 TACTACATATATATGCTTGCAACCAAGGAGAGTTTTATAAATATTCTTGGCTGGGAA 1184
 Db 541 CAGTGTGTTTATACGCTAGCTCCTAAGGGTGAATTTTACAACTACTCAGGATGCGAAA 600
 Qy 1185 TACCTTCAACTGTAATCATCTGTGGTTCGTCATTCATTTAGTAGATTTTGAAGTACTG 1244
 Db 601 TACCTTCAACTGTAATCAATCCATTGACGTCATTTATAGTGGATTTGCTTGAAGATTTG 660
 Qy 1245 GGTGACGGAATGATGTTGATGTTTGTGTTTGTGCTTGTGATCTTGCATCCATAATGACAGAG 1304
 Db 661 GGTACCGGAATGACGTAGATGCTTCCGCTTGTGATCTTGTGCTTCTATCTTACAAGAG 720
 Qy 1305 TTCCAGTCTGTGGGATCCAGTTAACGTTATGAGAGTCCCAATAGAGGTGACATGATCAC 1364

Db 721 TAGCAGCTCGTGAATGCTGTAAATGCTCTATGGAAATTCAAATTGACGGTGACATGATCAC 780
QY 1365 AACAGGACACCTCTTCTTACTCCACCACCTATTGACATGATCAGCAATGACCAATTCT 1424
Db 781 CACAGGACCTCTCTCAAGCCACCATTGATGATGATGATGATGATGATGATGATGATGAT 840
QY 1425 TGGAGGCGTCAAGCTCAATGCTGAAGCATGGGATGAGGAGGCTCTATCAAGTAGGTCA 1484
Db 841 TAGTGGAGTAAAGCTTATAGCTGAAGCATGGGATGAGGAGGCTTTTACCAAGTTGGCAT 900
QY 1485 ATTCCCTCACTGGAATCTTTGGTCTGAGTGGAAATGGGAAGTACCGGACATTTGGGTCA 1544
Db 901 GTTTCGCACTGGGATCTGCTCGGAGTGAACGGAAGTACCGTGAATGATGATGATGATGATGAT 960
QY 1545 ATTCATTAAAGGCACTGATGATTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1604
Db 961 GTTCATCAAGGCACTGATGGTCTTCTGGGCTTTTGGTGAATGCTTTTGGTGAAGCC 1020
QY 1605 ACACCTATACCAAGTATGTTGGTCACTATCTTGAATGATGATGATGATGATGATGATGATGAT 1664
Db 1021 AAATCTATACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1665 ATTTTATATATACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724
Db 1081 CGATGGTTTACTTTGGTCTGATTTAGTGACATACACAAATAACAAATTTGCAATGG 1140
QY 1725 ATATG 1729
Db 1141 AGAGG 1145

RESULT 11
AA34655
ID AA34655 standard; DNA; 9289 BP.
XX
AC AA34655;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Hexaploid wheat DBE genomic sequence.
XX
KW starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein 1; bacterial isomylase; glycogen synthase;
KW WSBE 1-D4 gene; ss.
XX
OS Aegilops tauschii.
XX
FH Key Location/Qualifiers
FT CDS 1..9287
FT /*tag= a
FT /note= "the start codon is not indicated; contains 146
FT internal stop codons"
XX
PN WO9914314-A1.
XX
PD 25-MAR-1999.
XX
PF 11-SEP-1998; 98WO-AU000743.
XX
PR 12-SEP-1997; 97AU-00009108.
XX
PR 20-MAR-1998; 98AU-00002509.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (AUSU) UNIV AUSTRALIAN NAT.
XX (GOOD-) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI Li Z, Morell M, Rahman S;
XX WPI; 1999-229525/19.
DR

DR P-PSDB; AAY06919.
XX New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisense sequences of granule bound synthase.
XX
XX Claim 14; Page 103-115; 171pp; English.
XX
CC The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC rice or maize. The methods and products can be used for targeting
CC expression specifically to the endosperm of the seeds of cereal plants
CC such as wheat or barley. They can be used for the expression of e.g.
CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.
CC wt. glutenin, grain softness protein 1, bacterial isomylase, bacterial
CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
CC used for modifying the characteristics of starch produced by a plant. The
CC present sequence represents the wheat DBE genomic DNA sequence. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 9289 BP; 2477 A; 1909 C; 2040 G; 2863 T; 0 U; 0 Other;
Query Match 17.8%; Score 533.4; DB 2; Length 9289;
Best Local Similarity 95.1%; Pred. No. 7.9e-105;
Matches 562; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 1 GGTCTGGGCGCGCGCGCGCGCTGCGACCGTGGCGAGCCCAATCCGACGGCGGGAAGGGG 60
Db 1943 GGCGCGCGCGCGCGCGCGCTGCGACCGTGGCGAGCCCAATCCGACGGCGGGAAGGGG 2002
QY 61 TCGGCGAGGTGTGCGCGCGCGGTTCGAGAGCGCGGCGACGAAGGTAGAGACAGAG--GGGG 117
Db 2003 TCGGCGAGGTGTGCGCGCGCGGTTCGAGAGCGCGGCGACGAAGGTAGAGACAGAG 2062
QY 118 AGGAGACGAGCCGCTGCGCGAGGACAGGTACGCGCTCGCGCGCGCGCTGCGAGGGTCTCG 177
Db 2063 ACGAGGAGGAGCGGTGCGCGAGGACAGGTACGCGCTCGCGCGCGCGCTGCGAGGGTCTCG 2122
QY 178 CCGGATGCGCGCGCGCGCTGCGCGCGCGCGCGCGCTGCGCGCGCGCGCTGCGCGCGCT 237
Db 2123 CCGGATGCGCGCGCGCGCTGCGCGCGCGCGCGCGCTGCGCGCGCGCGCTGCGCGCGCT 2182
QY 238 ATTCCGCGGAGCCACCGCGCGCGCTGCGCTCTTTCAGCCAGAGATCTCAAGCGG 297
Db 2183 ACTCCGCTGAGCCACCGCGCGCGCTGCGCTCTTTCAGCCAGAGATCTCAAGCGG 2242
QY 298 TGGGGTTGCTCCCGAGTAGATTTCATGAGCTTCGCTGCGCGCGCGCGCGCGCTTTTGG 357
Db 2243 TGGGGTTGCTCCCGAGTAGATTTCATGAGCTTCGCTGCGCGCGCGCGCGCGCTTTTGG 2302
QY 358 GCCTGCAATTTAAGTTTCTACTGGGCGAAATGCTGCGAGGATAGGTGACCGAGGAGTT 417
Db 2303 GCCTGCGATTTAAGTTTCTACTGGGCGAAATGCTGCGAGGATAGGTGACCGAGGAGTT 2362
QY 418 CCCCTTGACCCCTGATGAATCGGACCGGAAACGTTGCGCATGTCTTCATCGAAGCGAG 477
Db 2363 TCCCTTGACCCCTGATGAATCGGACCGGAAACGTTGCGCATGTCTTCATCGAAGCGAG 2422
QY 478 CTGCACAAATGCTTTACCGGTACAGGTTCGAGCGCACCTTTGCTCCCTCAGTCGCGGCAC 537
Db 2423 CTGCACGAATGCTTTACCGGTACAGGTTCGAGCGCACCTTTGCTCCCTCAGTCGCGGCAC 2482
QY 538 TACCTTGATGTTTCCAAATGCTGCTGGTGGATCCCTTATGCTTAAGCGCAGTGATA 588
Db 2483 TACCTTGATGTTTCCAAATGCTGCTGGTGGATCCCTTATGCTTAAGCGTGTATGATA 2533

RESULT 12
ADC08661
ID ADC08661 standard; DNA; 603 BP.
XX
XX ADC08661;
AC

RESULT 14	
ADC07811	
ID	ADC07811 standard; DNA; 432 BP.
XX	
XX	
AC	ADC07811;
XX	
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Rice DNA sequence Seq ID77 related to grain filling.
XX	
KW	plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW	carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW	tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW	wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;

174	GAAGATGAACGAAGGCGAGATCTACGTGGCCTTCA	CGCAGCCATTTCGCGCGGT	233
2726	TGTTGAGCTCCAGAGCGCGCAGGGCCCGGTGGAA	CCGGTGGTGGACACAGGCAAGCC	2785
234	TGTTGAGCTCCAGAGCGGCCAGGCTACCGCTGGAG	CCCGCTGGTGACACAGGCAAGCC	293
2786	AGCACCATACGACTTCTCTCACCGACGACTTACCT	GTATGGCGCTCTACCATACACCAAGTT	2845
294	AGCGCCTTATGACTTCTCTCACCGACGACCTGC	CTGATCGTGCTCAGCCGCTCACCTGTT	353
2846	CTGCGATTTCTCTACTCTGAACTCTATCCCATGCT	CATCTCATCTCGCTCATCTAGT	2905
354	CTCTCATTTCTCAACTCCCAATCTCTACCCCAATG	CTCAGTACTCTCCATCATCTCTTGA	413

Query Match	9.2%	Score 275;	DB 9;	Length 432;
Best Local Similarity	82.8%;	Pred. No. 1.8e-49;		
Matches 314;	Conservative	0;	Mismatches 65;	Indels 0;
Gaps 0;				

QY	2906	ATTGGCCCTGATGTTTGA	2924
Db	414	ATTGCAGCCTGATGTTGA	432
Db	8777	CTCTCATTTTCCTCAACTC	8836
		CCTATCTCTATCTCTATCT	TATCTCTAGCTCAGCTACT
QY	2906	ATTGGCCCTGATCTTTGAGAGACCAATATA	2938
Db	8837	ATTGGCCCTGATGTCTGAAGAAGCGGATACA	8869

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1008	33.6	2700	4	US-09-731-166-15	Sequence 15, Appl
2	1000	33.6	2712	2	US-08-410-784A-1	Sequence 1, Appl
3	673.2	22.5	2706	4	US-09-463-238-2	Sequence 2, Appl
4	613.2	20.5	2806	4	US-09-463-238-11	Sequence 11, Appl
5	575.4	19.2	2133	3	US-09-187-124-1	Sequence 1, Appl
6	575.4	19.2	2133	4	US-09-850-936-1	Sequence 1, Appl
7	149.2	5.0	2634	4	US-09-463-238-3	Sequence 3, Appl
8	143	4.8	1230025	4	US-09-138-452A-1	Sequence 1, Appl
9	129.6	4.3	1389	4	US-09-463-238-12	Sequence 12, Appl
10	120	4.0	2523	2	US-08-410-784A-3	Sequence 3, Appl
11	102.8	3.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl
12	102.8	3.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl
13	88.8	3.0	1830121	4	US-09-557-884-1	Sequence 1, Appl
14	88.8	3.0	1830121	4	US-09-643-990A-1	Sequence 3, Appl
15	80.6	2.7	2181	3	US-09-123-075-3	Sequence 3, Appl
16	80.6	2.7	2181	4	US-09-346-237-12	Sequence 12, Appl
17	80.6	2.7	2181	3	US-09-544-123-3	Sequence 3, Appl
18	80.4	2.7	2151	4	US-09-489-039A-3670	Sequence 3670, Ap
19	77.8	2.6	8151	4	US-09-253-911A-8201	Sequence 8201, Ap
20	77.8	2.6	972	4	US-09-253-911A-8102	Sequence 8102, Ap
21	77.8	2.6	1944	4	US-09-253-911A-8062	Sequence 8062, Ap
22	76.4	2.5	477	4	US-09-253-911A-7999	Sequence 7999, Ap
23	74	2.5	1671	4	US-09-253-911A-8261	Sequence 8261, Ap
24	70.4	2.3	1215	4	US-09-556-877-61	Sequence 61, Appl
25	70.4	2.3	1215	4	US-09-620-412C-61	Sequence 61, Appl
26	70.4	2.3	1215	4	US-09-410-568-61	Sequence 61, Appl
27	70.4	2.3	1215	4	US-09-598-419-61	Sequence 61, Appl

QY	379	CTGGGGCAAAATGCTGCAGGATAGGGTGACCGAGGAGGTTCCCTTGACCCCTGATGAAT	438
Db	450	-----GGATAGGGTGACCGAGGAGGTGCCCTCGATCCCTGCTCAAC	492
QY	439	CGGACCGGAACGTTGCGCATGTTCTTCAATCGAAGG---CGAGCTGCACAACATGCTTTTAC	495
Db	493	CGAACGGGAACGTTGGCGACGTTGTCATCCACCGGACCGAGCTGCACGGCATGCTCTAC	552
QY	496	GGGTACAGTTTCGACGGCACCTTTGCTCTCACTCGGGCACTACCTTGATGTTTCCAAAT	555
Db	553	GGATACAGTTTCGATGGCGTGTTCGCCCTGAGCGCGACAGTACTACGATGTGTCTCAAC	612
QY	556	GTCTGTGTGGATCCTTATGCTTAAGGCAGTGAATAAGCCGAGGGGAGTATGGTTCTCAAGG	615
Db	613	GTTGTGTGGATCATACGCTTAAGGCAGTGGTAAAGCCGAGGTGAATATGGTGTGCCCTGCG	672
QY	616	CGTGGTAACAATTGCTGGCCCTCAGATGGCTGGCATGATCCCTCTTCATATAGCACGTTT	675
Db	673	CCTGGTGGTAGTTGTTGGCCCTCAATGGCTGGTAGATCCCTCTCCCTATATAAGTTT	732
QY	676	GATTGGGAAGCGGACCTTACCTCTTAAGATATCCTCCAAAGGACCTGGTAAATATATGAGATG	735
Db	733	GATTGGCAAGTGACCTACCCCTTTGGGTACCATCAGAAGGACCTTGTCATATATGAATG	792
QY	736	CACTTGCGTGATTTCAGGAACATGATTCAGACATGTAGAACATCCGGGTACTTTCATT	795
Db	793	CATTGCGTGATTTCACAAACACACTCAAGCAAGACAAACACCAGGAACCTTACATT	852
QY	796	GGAGCTGTGTCGAAGCTTGACTATTTCGAAGGAGCTTGGAGTTAATGTATTGTAATTAATG	855
Db	853	GGTCTGTGTCAAAAGCTTGACCATCTAAAGGAACCTTGGAGTGAACCTGTATAGACTAATG	912
QY	856	CCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCTTCCAGATGAACTTTTGG	915
Db	913	CCCTGCCATGAGTTCAATGAGCTAGAGTACTTCAGCTCCCTCTTCGAAGATGAACTTCTGG	972
QY	916	GGATATTCTACCAATAAATCTCTTTTACCATAAGTACAAGATACACATCAGCGCGGATAAAA	975
Db	973	GGATATTCCAAATAAATTTTCTCACAAATGGCAAGATATCTTCAAGTGGCATGAAGA	1032
QY	976	AACGTGGGCGGTATGCCATAAATGAGTTCAAAACTTTGTGAAGAGGCTCACAAAACGG	1035
Db	1033	GACTCTGGATGTGTGCCATAAATGAATTAAGCTTTGTGAAGGAGGCCCCAACAAACGG	1092
QY	1036	GGAAATCGAGGTGATCCTGGATGTTGTTCTTCAACCATACAGCTGAGGGTAAATGGAATGGT	1095
Db	1093	GGAAATCGAGGTGATCATGGATGTTGTTCTTCAATCATACAGCTGAAGGTATGAGAAAGC	1152
QY	1096	CCAAATATTATCAATTAAAGGGGTCGATAATACTACATCTATATGCTTGACCCCAAGGA	1155
Db	1153	CCAAATATTATCCTTTAGGGGATAGATAATAGTACATACATGCTTGACCTTAAGGA	1212
QY	1156	GAGTTTATTAACATATCTGGCTGTGGATACCTTCAACTGTANTCATCTGTGTTTCT	1215
Db	1213	GAGTTTATTAATATCTGGTGTGGAAATACCTTCAATTTGAATCATCTGTAGTCCGT	1272
QY	1216	CAATTCAATGTAGATGTTTAAAGATACCTGGGTGACGGAAATGCAATGTATGATGGTTTCT	1275
Db	1273	GAAATTTATAGTGGATGCTTGGATACCTGGGTAAACAGAAATGCATGTGATGGTTTCT	1332
QY	1276	TTTGATCTTGGATCCATAATGACACAGAGTTCAGTCTGTGGATCCAGTTAAGCTGAT	1335
Db	1333	TTTGACCTTGCACTATACTGACACAGAGTATGAGTCTATGGGATCCAGTTAATGTGAT	1392
QY	1336	GGAGCTCCAAATAGAAGGTGACATGATCAACACAGGGACACCTCTTGTACTCTCACCACTT	1395
Db	1393	GGAAGTCCAAATGGAAGGTGACATGATTAACACAGGGACACCTCTTGTGTGCCCAACCTT	1452
QY	1396	ATTGACATGATCAGCAATGACCCCAATTTCTTGGAGCGGTCAAGCTCATCTGCTGAAGCATGG	1455
Db	1453	ATTGACATGATTAGCAATGACCCCAATTTCTTGGAAATGTCAAGCTCATCTGCTGAAGCATGG	1512

QY	1456	GATCAGGAGGCCCTCTATCAAGTAGGTCAATTCOCCTCACTGGAACTGTTTGGTCTGAGTGG	1511
DB	1513	GATCAGGAGGCTCTCTATCAAGTTGGTCAAGTTTCTCTACTGGAACTGTTTGGTCTGAGTGG	1572
QY	1516	AATGGGAAGTACCGGACATTTGCGTCAATTTCAATTAAGGCACTCATGGATTTGCTGGT	1575
DB	1573	AATGGAAGCTATCGCGATACCGTGGTCAAGTTTCAATCAAGGCAAGATGATTTGCTGGT	1632
QY	1576	GGTTTTCGCAATGTCTTTGTGGAAGTCCACACTATACGAGTAAGTTGTGCGCAATCT	1635
DB	1633	GCCTTTCGCAATGCCTATGTGGAAGTCCACAGTTATC	1671
QY	1636	TGTAATAGAGTTGAGTGCAATGTCACTCGGATTTTATATATACCAATGATGATACACA	1695
DB	1672	-----	1671
QY	1696	TCATAATATATAACAATCATAGTGTATGCATATGCAATTTGGCTAAGAAGTATTTAGTGTAT	1755
DB	1672	-----	1671
QY	1756	ACACTAGTCTATATATAGTGTTTAACAACCCACTTGCCAATGAAGCAATAGGCGTTT	1815
DB	1672	-----	1671
QY	1816	CTAGTTATCTTATTTATTTGTCCGGTGAATAATCCACTGAAAAATTCAGCCATGTCAAT	1875
DB	1672	-----	1671
QY	1876	TTTTAGGGGGAGAGAAACTATATGTATTTGCCCCCTAAAGAACCACTCTCAGAAAT	1935
DB	1672	-----	1671
QY	1936	TCATAGTAAGTTGCTTTTCTGTAAGAAAGGAACGACTTCATACACTTTCTATCGGTGC	1995
DB	1672	-----	1671
QY	1996	TAACTTAGCTCGATGATATATTTGAAGATGAATGCCAAATTTAAATTTGTGCGAATAATTG	2055
DB	1672	-----	1671
QY	2056	ATCTGTTATTCACAAATTTCTATTTGGTTCTCTAGAAATCAAAACAGTAACTTGTTAT	2115
DB	1672	-----	1671
QY	2116	GGCACTGCAACTTCTTATTGATTAATCAGCAGGAGGAAGGAACCTTGGCAGAGTATCA	2175
DB	1672	-----CAGGCGGGGGAGGAAGCCTTGGCAGAGTATCA	1705
QY	2176	ACTTTGTATGTGCATATGATGGATTTTACACTGGCTGATTTGTGTAAATATATAGAAGT	2235
DB	1706	ACTTTGTATGTGCACAGATGGATTTTACACTGGCTGATTTGTGTACATCAATATAGCAAGT	1765
QY	2236	ACAATTTACCAATGGGAGAACACAGAGATGGAGAAAATCACAATCTTAGCTGGAAT	2295
DB	1766	ACAATTTGTCAATGTGTAGGACACAGAGATGGGGAATCATATCTTAGCTGGAAT	1825
QY	2296	GTGGGAGGAAGAGAAATTCGCAAGATGTGTGTCAAAAGATTGAGGAAGAGCGCATGC	2355
DB	1826	GTGGGAGGAAGAGAAATTTGCAAGTCTGTAGTCCGAAGATTAAGGAAGAGGCAATGC	1885
QY	2356	GCAATTTCTTTGTTCTCATGTTTCTCAGGAGTTCCAAATGTTCTACATGGGTGATG	2415
DB	1886	GCAATTTCTTTGTTCTTAUGTTTCTCAGGAGTTCCAAATGTTCTACATGGGCGATG	1945
QY	2416	AATATGCCACACAAAGGGGGCAACAATACATATGCCATGATTTCTTATGTCAAT	2475
DB	1946	AATATGTCACACAAAGGGAGGAACAAACATACGTACTGCCATGACCAATATGTCAACT	2005
QY	2476	ATTTTTCGCTGGGATAAAA---AAGAACATATCTGTAGTTGCACCGATTTCTGCTGCTCA	2532
DB	2006	ATTTTCGTTGGGATAGAAGGAAGAACATCTCTGATTTGTACAGATTTCTGCCGTTCTCA	2065
QY	2533	TGACCAAAATTCGCCAAGAGTGCAGGGTCTTTGGCCTTCAGAGACTTTTCCAAAGGCCAAAC	2592

; CURRENT APPLICATION NUMBER: US/09/463,238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2641)
; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-2

Query Match 22.5%; Score 673.2; DB 4; Length 2706;
Best Local Similarity 69.4%; Pred. No. 3.3e-149;
Matches 937; Conservative 0; Mismatches 398; Indels 15; Gaps 1;

QY 395 AGGATAGGAGTACCGAGGAGTTCCTTGCACCCCTGATCAATCGACCGGAGCGGTGT 454
DB 425 AGAAGAGAGTGACCGAGCAAAATTTCTCGATCCTCTAGCTAATAAACTGGAGATGTAT 484
QY 455 GGCATGCTTCATCAAGGCGAGCTGCACACATGCTTTACGGGTACAGGTTGACGGCA 514
DB 485 GCGATGTTCTCTTAAGGGAGATTTGAGAATATGCTATATGCTACAAATTTGATGGGA 544
QY 515 CTTTGTCTCTCACTGCGGGGACCTACCTTGATGTTTCCATGTCGTTGATGCTTTATG 574
DB 545 AATTCTGTCTCTGAAGAGGACACTACTTTCGATCTTCCGAGATAGTGTTCGATCCTTATG 604
QY 575 CTAAGGCGAGTGATAAGCGGAGGATGTTGTTTCCAGCGGTGGTAACTTGTCTGGC 634
DB 605 CCAAGGCTATAGTAAGCAGAGGAGATATGTTGTTATAGGCCAGAGGTGATTTGTGGC 664
QY 635 CTCAGATGGCTGGCATGATCCTCTTCCATATAGCAGCTTTGATGTTGGAAGGCGACCTAC 694
DB 665 CCCCAATGGCTGGCATGCTTCTGCTTCTGATCAGTTTGAATGGGAAGGAGATCTAC 724
QY 695 CTCATAGATATCTCTCAAGGACCTGGTAAATATATATAGATGCACTTGCCTGGATTCACGA 754
DB 725 CACTGAGTTTCCACAGAGATCTTGTAACTTAAGTAAGTAAGTATGTTGGGTCTTACTA 784
QY 755 AGCATGATTCAAGCAATGTAGAACATCCGGTACTTTTCATTTGGAGCTGTGTGCAAGCTTG 814
DB 785 ATCATGAGTCGAGTGAACAAATATCTCTGCTACTTACCTTGGTGTGTTGGAGAACTTG 844
QY 815 ACTATTTGAAGGACTTGGAGTTAATGTTATTAATTAATGATCCCTGCGCATGAGTTCAACG 874
DB 845 ATCACTTGAAGGAATCTGGTGCACCTGTATAGAGCTAATGCCCTGTCACGAGTTCAATG 904
QY 875 AGCTGGAGTACTCAACCTCTCTTTC-----CAAGATGAACTTTTGGGGAT 919
DB 905 AGCTGGAGTACTATAGTTAATACTCTGTATTTGGCGACTACAAGTTTAACTTTTGGGCT 964
QY 920 ATTCTACATAAACTCTCTTTTCAATGACAGATACATCATCAGGCGGATATAAAACT 979
DB 965 ATTCTACTGCAATTTCTCTTCTCAATGGGAAGATACATCTCTGCTGTCTAAGTAAT 1024
QY 980 GTGCGGCTGATGCCATAAACTAGTTTCAAACTTTTGAAGAGAGGCTCACAAAGGGGAA 1039
DB 1025 CGCGCTCGGTGCAATAAAGAAATTAAGTATCTGTCAAGGAAGCACATAACGTGGA 1084
QY 1040 TTGAGGTGATCCTGGATGTTGCTTCAACCATACAGCTGAGGTAATGAGATGTTCCAA 1099
DB 1085 TCGAGGTATCATGGATGTTGTTTCAATCACTGCTGAAGGAATGAAATGTTCCCA 1144
QY 1100 TATTATCAATTTAAGGGGTGATTAATCTATACATATATGCTTGCACCCCAAGGAGAT 1159
DB 1145 TACTATCATTTAGAGGCATTGACAACTAGTGTTTATACGCTAGCTCTCTAAGGGTGAAT 1204

QY 1160 TTTTAACTATTCTGGCTGTGGGAATACCTTCAACTGTAATCATCTCTGTGGTTCGTCAAT 1219
DB 1205 TTTTCACTACTCAGGATGTGGAATACCTTCACTGTAATTAATCCCATTTGACGTCAAT 1264
QY 1220 TCATTGTAGATTTTAAAGATACTGGGTGACGGAATGATGTTGATGTTTTCGTTTGT 1279
DB 1265 TTTATAGTGGATTGCTTGAGATATTGGGTTACCGAAATGACGTAGATGGCTTCCGCTTTG 1324
QY 1280 ATCTTGCATCAATATGACAGAGGTTCCAGTCTCTGGGATCCAGTTAACTGATGGAG 1339
DB 1325 ATCTTGTCTTCTATCTTACAGAAAGTAGCAGCTCTGGAATGCTGTAATGCTTATGGAA 1384
QY 1340 CTCCAATAGAGGTGACATGATCAACAGGAGGACACCTCTCTTACTCCACCACCTATTG 1399
DB 1385 ATTCAATTGACGTTGACGTGATCACCACAGGACCTCTCTCACAAGCCACCATTGATG 1444
QY 1400 ACATGATCAGCAATGACCAATTTCTTGGAGGCGTCAAGCTATTTCTGTAAGCATGGATG 1459
DB 1445 ATATGATTAGCAATGATCCAATACTTCTGGGAGTAAGCTTATAGCTGAAGCATGGGAT 1504
QY 1460 CAGGAGGCTCTATCAAGTAGTCAATTCCTCCTCACTGGAAATGTTTGGTCTGAGTGGAA 1519
DB 1505 GTGGAGGCCCTTTACCAAGTTGGCATGTTTCCGCTATGGGTATCTGGTGGAGTGGAA 1564
QY 1520 GGAAGTACGGGACATTTGCGTCAATTCATTTAAAGGCACTGATGATTTGCTGGTGGTT 1579
DB 1565 GAAAGTACCGTACATGTTGACGCGAGTTTCACTCAAGGCACTGATGGGTTTCTGGGGCTT 1624
QY 1580 TTGCGCAATGCTTTTGGAGTCCACACCTATACAGGTAAGTTGTGCAATATCTTGT 1639
DB 1625 TTGCTGAATGCCCTTTGTGGAAGCCCAATCTATACAGAAAGGAGGAAGAAACCATGGA 1684
QY 1640 AATGAGTTGAGTGAATGTCACTGGATTTTATATATATACCATGATGATACATCTA 1699
DB 1685 ACAGTATAAATTTCTGTGTGCGCCAGATGGTTTACTTTGCTGATTTAGTGACATACA 1744
QY 1700 AATATATAACAATCATAGTGTATGATGATG 1729
DB 1745 ACAATAAACACAAATTTGGCAATGGAGG 1774

RESULT 4

US-09-463-238-11
; Sequence 11, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Alison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463,238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (822, 826, 2707 and 2797)
; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-11

Query Match 20.5%; Score 613.2; DB 4; Length 2806;

Best Local Similarity 68.0%; Pred. No. 4.9e-135; Matches 922; Conservative 0; Mismatches 410; Indels 24; Gaps 4;

QY 395 AGGATAGGGTACCGAGGAGGTTCCCTTTCACCCCTTGATGAATCGGACCGGGAACGTGT 454
Db 488 AGAAGAGGTACCGAGGAGGTTCCCTTTCACCCCTTGATGAATCGGACCGGGAACGTGT 547
QY 455 GGCATGCTTCATCGAAGGCGAGTGCACAACTGCTTTACGGGTACAGGTTTCGACGGCA 514
Db 548 GGCATGCTTCATCGAAGGCGAGTGCACAACTGCTTTACGGGTACAGGTTTCGACGGCA 607
QY 515 CCTTTGCTTCCTCACTGCGGGGACCTTTCATGCTGCTTCCCAATGCTGCTGCTGCTTATG 574
Db 608 AATTCTGCTCTGAAGAGGACACTTTCGACTCTTCGCGAGATGTTGGATCCCTTATG 667
QY 575 CTAAGGCGATGATAAGCGGAGGAGTATGTTTCCAGCGGCTGGTGAACATTTGCTGGC 634
Db 668 CCAAGGCTATAGTAAGCAGAGGAGATATGTTGTTAGGCGCAGAGGATGATTTGTTGGC 727
QY 635 CTCAGATGGCTGGCATGATCCCTCT--TCCATATAGCAGCTTTGATTGGGAAGGCGACC 691
Db 728 CCCAATGGCTGGCATGATGATCCCTCT--TCCATATAGCAGCTTTGATTGGGAAGGAGATC 787
QY 692 TACCTCTAAGATATCTCTCA---AAAGACCTGGTGAATATATAGATGACCTTCGCTGGAT 748
Db 788 TACCACCTGGAAGTTTCCACAGAGAGATCTTGTATATCATGAAATCGATGTTTCGTGGGT 847
QY 749 TCAGGAGCATGATTCAGCAATGTAGAACTCGGCTGCTTTCATTTGAGGCTGTGCGA 808
Db 848 TTACTATCCATGAGTCAGTGAACAAATATCTCGTACTTACCTTTGGTGTGGAGA 907
QY 809 AGCTTGACTATTTGAAGGAGCTTGGAGTTAATTGTTTGAATTAATGCCCTGCGCATGAGT 868
Db 908 AACTTGATCACTTGAAGGAACCTTGGTGTCAACTGTATAGAGTAATGCTCCCTGTACAGAGT 967
QY 869 TCAAGGAGCTGGAGTACTCAACTCTCTCTC-----CAAGATCAACTTTT 913
Db 968 TCAATGAGCTGGAGTACTATAGTTATTAATCTGTAATGGCGACTCAAGTTTAACTTTT 1027
QY 914 GGGATATCTTACCAATAAATCTTTTCCAAATGACAGATACACATCAGGCGGATAA 973
Db 1028 GGGCTATCTACTGTCAATTTCTTTTCCAAATGGAAGATCTATCTGCTGCTTAA 1087
QY 974 AAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGAAGAGGCTCAAAAC 1033
Db 1088 GTAATTCGGCTCGGTGCAATAAAGAAATTAAGTATCTTGTCAAGGAAGCACATAAAC 1147
QY 1034 GGGGAATTTAGGTGATCTCTGATGCTCTTCAACCATACAGCTGAGGGTAATGAGAATG 1093
Db 1148 GTGAATTCGAGGTTATCATGATGTTGTTTCAATCATCATGCTGAAGGAATGAATG 1207
QY 1094 GTCCAAATATATCAATTTAAGGGGTGCGAATAACTACATACTATATGCTTTGCCACCAAGG 1153
Db 1208 GTCCCACTATATCTTTAGAGGCAATTCACAACTGTTTATACGCTAGCTCCTTAAGG 1267
QY 1154 GAGAGTTTATTAATCTATCTGGCTGGGATACCTTCACTGTATCATCTGCTGTTTC 1213
Db 1268 GTGAATTTTCAACTACTACAGGATGTGGAATAACCTTCACTGTATTAATCCCATTTGTAC 1327
QY 1214 GTCAATTCATTTAGATTTGTTTAAAGTACTGGGTGACGGAATGCAATGTTGATGTTTTC 1273
Db 1328 GTCAAT---TTATAGTATGCTGAGATATTGGGTTACGGAATGCACTACATGGCTTCC 1384
QY 1274 GTTTTGATCTTGGATCCATTAATGACAGAGGTTCCAGTCTGTGGGATCCAGTTAACTGT 1333
Db 1385 GCTTTGATCTTGTCTTATCTCTTACAAGAAAGTAGCAGCTCGTGGAAATGCTGTAATGTCT 1444
QY 1334 ATGGAGCTCCAAATAGAAGGTGACATGATCAACAGGGGACACCTCTTGTGTACTCCACCAC 1393
Db 1445 ATGGAATTCNAATTGACGGTGAAGTATCAACAGGCACTCTCTCTCAAGGCCCACTAT 1504
QY 1394 TTATTTGATGATCAGCAATGAGCCCAATCTTGGAGGCGTCAAGCTCATTTGCTGAAGCAT 1453

Db 1505 TGATTGATGATTAGTCAATGATCCAACTACTTCGTGGAGTAAAGCTTATAGCTGAAGCAT 1564
QY 1454 GGGATGCGAGGAGGCTCTTATCAAGTAGTCAATTCCTCCTCACTGGAATGTTTGGTCTGAGT 1513
Db 1565 GGGATTTGGAGGCGCTTTTACCAAGTTGGCATGTTTCCGCACCTGGGTATCTGGTGGAGT 1624
QY 1514 GGAATGGGAAGTACCGGACATTTGGCTCAATTCATTAAAGGCACTGATGGAATTTGCTG 1573
Db 1625 GGAACGGAAGTACCGTGACATGTTACCGGAGTTTCAACAGGCACTGATGGGTTTCTG 1684
QY 1574 GTGGTTTGGCCAAATGCTTTTGTGGAAGTCCACACCTATACCAAGTAAGTTGTGGCAATA 1633
Db 1685 GGGCTTTTGTCTGAATGCTTTTGTGGAAGCCCAATCTATACCAAGAGGAGGAGAAAC 1744
QY 1634 CTGTAAATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCACTGATGATACA 1693
Db 1745 CATGGAACAGTATAAATTTCTGTGTGTCACAGATGTTTACTTTGGCTGATTTAGTGA 1804
QY 1694 CATCTAAATATATACCAATCATAGTGTATGCAATG 1729
Db 1805 CATACAACATAAACAATTTGGCAATGGAGAGG 1840

RESULT 5
US-09-187-124-1
; Sequence 1, Application US/09187124A
; Patent No. 6255563
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossman, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; TITLE OF INVENTION: FROM POTATO
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/187,124A
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: PCT/EP97/02292
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: DE 196 18 125.9
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1819)
; OTHER INFORMATION: Clone: Isos5
US-09-187-124-1

Query Match 19.2%; Score 575.4; DB 3; Length 2133;
Best Local Similarity 69.8%; Pred. No. 3.6e-126;
Matches 799; Conservative 0; Mismatches 331; Indels 15; Gaps 1;

QY 600 GTATGCTTTCAGCGGCTGTTGATTTGGGAAGGCGACCTACCTCTTAAGATATCCTCAAAAGGACCT 719
Db 1 GAATTCGGCAAGGCGGCGAGGATGATTTGGCCCCCAATGGCAGCATGTCACCTTC 60
QY 660 TCCATATAGCAGCTTTGATTTGGGAAGGCGACCTACCTCTTAAGATATCCTCAAAAGGACCT 719
Db 61 TCTTCTCATCAGTTTGTATTTGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGATCT 120
QY 720 GGTAAATATAGATGACATTTGGGTTTCCAGAGCATGATTTCAAGCATGTAGAAC 779
Db 121 TGTAACTATGAATGCAATGCTTGTGGGATTTCAAAATCATGAGTCGAGTGAACAAATA 180
QY 780 TCCGGGTACTTTCATTGGAGCTGTCTCGAAGCTTGACTATTTTGAAGGAGCTTTGAGTTAA 839
Db 181 TCCTGTACTTACCTTGTGTTTGGGAGAACTTTGATCACTTTGAAGGAACCTTGGTGTCAA 240
QY 840 TTGTTTGAATTAATGCTCCCATGAGTTTCAACAGCTGAGTACTCAACCTCTTCTTC 899

[illegible]

RESULT 7

US-09-463-238-3
; Sequence 3, Application US/09463238

; Patent No. 6469230
; GENERAL INFORMATION:

APPLICANT: Edwards, Smith

APPLICANT: SMITH, JAMES
APPLICANT: BUSTOS, JUAN

; APPLICANT: Martin,
; APPLICANT: Plant B

1. TITLE OF INVENTION: FILE REFERENCE: 97

FILE REFERENCE: 97-
CURRENT APPLICATION

; CURRENT FILING DATE
; PRIOR APPLICATION NO

PRIOR FILING DATE:
 PRIOR APPLICATION NO:

10; PRIOR FILING DATE: 10/1/2010

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; NUMBER OF SEQ ID NOS
;
; SOFTWARE: PatentIn v

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; SEQ ID NO 3
; LENGTH: 2634

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LENGTH: 2034
TYPE: DNA
ORGANISM: *Salmonella*

US-09-463-238-3

Query Match

Best Local Similarity
Matches 633. Conserved

Matches 633; Conser-

Qy 412 GAGGTTCC

Db
434 GAAATTAGC

Qy 472 GCGAGCTC

Query Match 5.0%; Score 149.2; DB 4; Length 2634;
Best Local Similarity 51.0%; Pred. No. 1.6e-25;
Matches 633; Conservative 0; Mismatches 508; Indels 99; Gaps 8;

412	GAGTTCCCTTGACCCCTGATGAATCGGACGGAAACGTGTGGCATGCTTTCATCGAA	471
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434	GAATTAGCATTTGATCCACAGAAGAACCCACAGGAGACATATGGCACATATGCAATTAAG	493
Db		
472	GGGAGCTGCA---CAACATGCTTTACGGTACAGTTTCGACGGACACCTTTGCTCTCAC	528
Qy		
494	GAGTTCCCAAGGTGGTGTCTTTATGGTTATTCGCATTCATGGACCTCGAAATTGGCAT	553
Db		
529	TGGGGGCATACCTTGATGTTTCCATATGTCGTGGTGGATCCATTATCTAAGGCATGATA	588
Qy		
554	GAAGGCGCATCGATTTGATGATGACATATTTTGGTTGATCCCTTACGCAAACTAATTGAA	613
Db		

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RESULT 8
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(15000)
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Query Match 4.8%; Score 143; DB 4; Length 1230025;
Best Local Similarity 55.3%; Pred. No. 7.5e-23;
Matches 359; Conservative 0; Mismatches 260; Indels 30; Gaps 3;

QY 671 CGTTTGGTGGAGGCGACCTACCTCTAAGATATCTCAAAAGGACCTGGTAATATATG 730
DB 446195 CATTTCTTGGATGGTATCAGCCCTGCTATTCGGAAGAGAGATGATCATCTATG 446254
QY 731 AGATGCACTTGGTGGATTCAGAGCATGATTCAGAGCATGAGTAAATTCGGTACTT 790
DB 446255 AGATGCACTGATGCTTCCTTCCACGCAATCTTCTCATCTAGGGTTCATGTCCGGGAACCT 446314
QY 791 TCATTGGAGCTGTCTCAAGCTTGACTATTGGAAGGAGCTTGGAGTTAATTGATTGAAT 850
DB 446315 TCCTAGGATCATTTGAAAGATCGACCATCTGCTAAGCTGGGAATCAACGCTGTGTGAC 446374

; 851 TAATGCCCTGCCATGAGTTCAACGAGCTGGAG-----TACTCAACCTCTCTTT 898
; 446375 TCTTACCTATCTTTGAGTTGATGAGACTGGCATCTCTTTTAGAAATTCGAATTCCTTT 446434
; 899 CCAAGATGAACCTTTTGGGGATATTCTACCAATAAACTTCTTTTCCAAATGACAAGATACA 958
; 446435 ATCTGTGCAATATTGGGGTTATGCTCCCTAAATTTCTTTTCTCTTGGCGAGCTTATG 446494
; 959 CATCAGGGGGGATAAAACACTGTGGCGCTGATGCCATAAATGATTCGAATCTTAAACTTTGTAA 1018
; 446495 CTTATGCC-----TCTGATCCTTGGCTCCCAAGTAGAGAGTTTAAAACTTTAGTAA 446545
; 1019 GAGAGGCTCAAAACGGGGAATTTGAGGTGATCCTGGATGTTGTCTTCAACCATACAGCTG 1078
; 446546 AGACCTTGCATCAAGAAGTATTGAGGTCAATCTTTGATGTTGTTTAAATCATACGGCT 446605
; 1079 AGGTAATGAGATGGTCCCAATATTATCATTTAAGGGGGTGCATAATACATACATACTATA 1138
; 446606 TGC-----AAGGGACGACCTGCTCTTTGCTTGGATAGACACTCCGAGCTATTATA 446656
; 1139 TGCITGCACCAAGGAGAGTTTATTAATACTATTCTGGCTGTGGGAATACCTTCAACTGTA 1198
; 446657 TTTTAGATGCACAGGTGCATTTTACAATTAATTCAGCTGTGGAAACACTCTCAATACAA 446716
; 1199 ATCATCCTGTGGTTCGTCATTAATTCATTTGATGTTTAAAGATATCTGGGTGACGGAATGC 1258
; 446717 ACCGGCCCCCACCAGCAATGGATTTCTCGACATCTTACGTTATTGGGTAGAGAAATGC 446776
; 1259 ATGTTGATGTTTCTGTTTTCATCTTGCATCCATAATGACCAGAGGTTTC 1307
; 446777 ATGTCGATGGGTTCGATTTGATCTTCTGCTTTCTTCTGCTGCTGCTC 446825

RESULT 9
US-09-463-238-12
; Sequence 12, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Allison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Search Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463.238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-09-463-238-12

Query Match 4.3%; Score 129.6; DB 4; Length 1389;
Best Local Similarity 53.0%; Pred. No. 5.2e-21;
Matches 357; Conservative 0; Mismatches 259; Indels 18; Gaps 3;

QY 2155 GGAACCTTGGCAGCATGATCAACTTTGATGTCACATGATGGATTTTACACTGGCTGATT 2214
DB 474 GAAAGCCGTACCAAGTGTCAACTTCGTGATTCGCCCATGATGGCTTTTACCTTTGATGACC 533
QY 2215 TGGTAACATATAATAAGAAGTACAAATTTACCAATGGGGAGAACCAACAGAGATGGAGAAA 2274
DB 534 TTGTTTATACAAATAAAGCAACATGATGCAACGGTGAAGGTGGCAATGATGATGCA 593
QY 2275 ATCAATCTTAGCTGGAATTTGGGGAGGAGAGATTCGCAAGATTTCTCTGTCAAAA 2334

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QY 2263 GAGATGAGAGAAATCAAACTTCTAGCTGGAATTTGGGGAGGAGGAGAAATTCGCAAGAT 2322
DB 1770248 GCGACGGGGAAGCTACACCGATCTGGAACTCGCGTGTGAGGGCCCAACCGATGACC 1770189
QY 2323 TGTCTGTCAAAAGATTTAGGAGAGGAGGAGATGCGCAATTTCTTTTGTCTCATGGTTT 2382
DB 1770188 CCGACATCTTGGCGCTGCTGCCGCCAGATGCGCAACATGTGGGCCACGCTTATGGTCA 1770129
QY 2383 CTCAGGAGTTCCAAATGTTCTACATGGTGTATGAATATGCGCACACAAAGGGGGCAACA 2442
DB 1770128 GCCAGGGCACCCGATGATGCCACCGGAGGAGATTGGCGACCCAAATACGGCAACA 1770069
QY 2443 ACAATACATAGTCCGATGATCTTTATGTCAATTTTTCGCTGGGATFAAAAAAGACAAT 2502
DB 1770068 ACAACGTCTAGTCCGAGGACTCCGAATTTCTTGGATGATTTGTCATTTGGTGACAAGA 1770009
QY 2503 ACTCTGAGTTGCCCGGATTTCTGCTCATGACCAAAATTCGCAAGGAGTGGAGGGTC 2562
DB 1770008 ATGCCGATCTGCTAGCTTTGCGACGAAGGCGAGCTTTGGCGAAGAACCAAGGTGT 1769949
QY 2563 TTGGCC 2568
DB 1769948 TTGGCC 1769943

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 3.4%; Score 102.8; DB 3; Length 4411529;
Best Local Similarity 52.6%; Pred. No. 4.1e-13;
Matches 224; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
QY 2143 AGGACGAGGAGAAACCTTTGGCACAGTATCACTTTGTATGTGCAATGATGATTTA 2202
DB 1770242 AAGCAACCGCGCGCGCCAGTCCAGTATCAATTTCTGTCACCGCCACGACGGTTCA 1770183
QY 2203 CACTTGGCTGATTTCTGTAACATATATAGAGTACATTTTACCAATGGGGAGCAACA 2262
DB 1770182 CACTCAACGACCTGTTCTGTAACGACAGCAACAGAGGCAATGGCGAGAACACC 1770123
QY 2263 GAGATGAGAGAAATCAACAATTTAGCTGGAATTTGTGGGAGGAGGAGAAATTCGCAAGAT 2322
DB 1770122 GCGACGGGGAAGGCTACACCGATCTGGAATCTGCGTGTGCGAGGGCCCAACCGATGACC 1770063
QY 2323 TGTCTGTCAAAAGATTTGAGNAGGAGGAGATGCGCAATTTCTTTTGTCTCATGGTTT 2382
DB 1770062 CCGACATCTTGGCGCTGCGTGGCCCGCCAGATGCGCAACATGTGGGCCACGCTTATGGTCA 1770003
QY 2383 CTCAGGAGTTTCCAAATGTTCTTACATGGGTGATGAATATGGCCACACAAAAGGGGGCAACA 2442
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DB 1769942 ACAACGTCTACTGCGCAGGACTCCGAATTTATCTTGGATGGATTCATTTGGTGACAAGA 1769883
QY 2503 ACTCTGAGTTGACCGATTTCTGCTCATGACCAATTTCCGCAAGGAGTGGCGGGTC 2562
DB 1769882 ATGCCGATCTGCTAGCTTTGCGACGCAAGGCGAGACCTTGGCAAGAACCACAAGGTGT 1769823
QY 2563 TTGGCC 2568
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RESULT 13
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PBI86P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 3.0%; Score 88.8; DB 4; Length 1830121;
Best Local Similarity 56.0%; Pred. No. 5.6e-10;
Matches 168; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
QY 987 TGATGCCATAATGAGTTCAAAACCTTTTGTAAAGAGGCTCACAAACGGGAATTTAGGT 1046
DB 1439162 TAATCCATTTGGTGAATTTAAACGATGCTAAAGGCATTTTCAAAAGCAGGCATTGAAT 1439221
QY 1047 GATCTGTGATGTTCTTCAACCATACAGCTGAGGTAATGAGATGCTCCAAATATTATC 1106
DB 1439222 TATTTAGACGTGGTATTTAACCATTCGCGAGATCGAGCAAACTTACCCACATTCAG 1439281
QY 1107 ATTTAAGGGGTTCGATAATCTACATCTATCTATCTTTCACCCCAAGGAGAGTTTATAA 1166
DB 1439282 CCAGCGTGTATTGATGATCAAACTTACTATTTCGCGCAACGATCAAGGCGCTTATATCAA 1439341

QY 1167 CTATTCGGCTGGGAATACCTTCAACTGTAATCATCTCCTGGTTCGTCAATTCATTGT 1226
Db 1439342 TTGACAGGCTGGCGCAATATGCTCAATTTATCCTCTGATAGGGCGAAATGGGTGGT 1439401
QY 1227 AGATTGTTTAAAGATACTGGGTGACGAAATGCAATGTTGATGGTTCGTTTTCATCTTGC 1286
Db 1439402 GGAATGCTGGTTATTGGGTGGAGCAATGCCATATTGATGGATTCCGTTTTCATTAGC 1439461

RESULT 14

US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

; GENERAL INFORMATION:

; APPLICANT: Robert D. Fleischmann

; Mark D. Adams

; Owen White

; Hamilton O. Smith

; J. Craig Venter

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville,

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,990A

; FILING DATE: 23-Aug-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/487,429

; FILING DATE: 1995-06-07

; APPLICATION NUMBER: 08/426,787

; FILING DATE: 1995-04-21

; ATTORNEY/AGENT INFORMATION:

; NAME: Kenley K. Hoover

; REGISTRATION NUMBER: 40,302

; REFERENCE/DOCKET NUMBER: PBI86P1C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5790

; TELEFAX: 310-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 3.0%; Score 88.8; DB 4; Length 1830121;

Best Local Similarity 56.0%; Pred. No. 5.6e-10;

Matches 168; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 987 TGATGCCATAATGAGTTCAAACCTTTTGTAAAGAGAGGCTCACAAACGGGGAATTGAGGT 1046

Db 1439162 TAATCCATTGGCTGAATTTAAACGATGGTAAAGGCATTTTCAAAACGAGGCATTGAAGT 1439221

QY 1047 GATCCTGATGTTGTCCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCATATTATC 1106

Db 1439222 TATTTAGCGTGGTATTAAACCATTCGCGAATCAGAGCAAACTTACCCACATTCAG 1439281

QY 1107 ATTTAAGGGGTGCGAATAATACTACATACTATATGCTTGCACCCAAAGGAGAGTTTATAA 1166

Db 1439282 CCAGCGTGGTATGATGATCAAACTTACTATTGGCGCAACGATCAAGGCGTTATATCA 1439341
QY 1167 CTAATTCCTGCTGGGAATACCTTCAACTGTAATCATCTCCTGGTTCGTCAATTCATTGT 1226
Db 1439342 TTGACAGGCTGGCGCAATATGCTCAATTTATCCTCTGATAGGGCGAAATGGGTGGT 1439401
QY 1227 AGATTGTTTAAAGATACTGGGTGACGAAATGCAATGTTGATGGTTCGTTTTCATCTTGC 1286
Db 1439402 GGAATGCTGGTTATTGGGTGGAGCAATGCCATATTGATGGATTCCGTTTTCATTAGC 1439461

RESULT 15

US-09-129-075-3

; Sequence 3, Application US/09129075

; Patent No. 6087149

; GENERAL INFORMATION:

; APPLICANT: Tsutsumi, No. 6087149iko

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Svendsen, Allan

; TITLE OF INVENTION: Starch Conversion Process

; FILE REFERENCE: 5262 204-US

; CURRENT APPLICATION NUMBER: US/09/129,075

; CURRENT FILING DATE: 1998-08-04

; EARLIER APPLICATION NUMBER: 0787/97

; EARLIER FILING DATE: 1997-07-02

; EARLIER APPLICATION NUMBER: 60/055,867

; EARLIER FILING DATE: 1997-08-13

; EARLIER APPLICATION NUMBER: PCT/DK98/00304

; EARLIER FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2181

; TYPE: DNA

; ORGANISM: Rhodothermus marinus

US-09-129-075-3

Query Match

2.7%; Score 80.6; DB 3; Length 2181;

Best Local Similarity 49.6%; Pred. No. 2.3e-09;

Matches 206; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 2172 ATCACTTTGTATGTGCACATGATGGATTACACTGGCTGATTTGGTAACATATAATAG 2231

Db 1378 ATCACTTCGTACCGCGCACACGCGCTTCACGCTGGAAGACCTGGTCAGCTACACGAAA 1437

QY 2232 AAGTACAATTTACCAATGGGAGAAACACAGAGATGGAGAAATCACAATCTTAGCTGG 2291

Db 1438 AAGCACACGACGAGCTGTAAGGCAACCGGACGCGCATGGACGAAACTACACGACG 1497

QY 2292 AATTGTTGGGAGGAGGAGAAATTCGCAAGATTGTCTGTCAAAGATTGAGGAAGGCGAC 2351

Db 1498 AACTGCGGGTGGAGGACCCACGAGGATCCGTCCTGCTGGCCCTGCGGGAAGCGCTC 1557

QY 2352 ATGCGCAATTTCTTTTGTCTCATGTTTCTCAAGGAGTTTCCAAATGTTCTACATGGGT 2411

Db 1558 AAGCGAGCTGATCAGCAGCTCTTTCTCTCGAGGGTGCCTCATGCTGCTGGCGCGC 1617

QY 2412 GATGATATATGGCCACACAAAAGGGGCAACAAATACATACATCTGCCATGATTTTATGTC 2471

Db 1618 GACGAGCTGTCGCGACGCGACGACGCGCAACAAACGCGCTATTGCCAGCAACAGAGATC 1677

QY 2472 AATTATTTTCGTTGGGATATAAAGAACAACTACTGTGATTCACCGGATTTCTGCTGCCTC 2531

Db 1678 AGCTGTACAACTGGCGAGCTTCACACGCGCAAGAGCAGATTTCTGGAGTTCGTGGCGCAG 1737

QY 2532 ATGACCAAAATTCGCAAGGAGTTCGAGGGTCTTGGCCCTTGAGGACTTTCACACGG 2586

Db 1738 ACGATCTGGTTTTCGACGAGCATCGAGCTTCGCGCGCGCCCAATTTCTGACCG 1792

Search completed: August 9, 2004, 22:08:05

Job time : 237 secs

2041	Db	TTGTGGGTAATTTGATCTGTATTATCAAAATTTCTATTGGTTTCTCTAGAAATCAAAAC	2100
2101	Qy	CAGTAACTTGTATTGGCACTGCAACTTCTTATTGATTAATACAGCAGGAGGAGGAAGAAC	2160
2101	Db	CAGTAACTTGTATTGGCACTGCAACTTCTTATTGATTAATACAGCAGGAGGAGGAAGAAC	2160
2161	Qy	CTTGGCACAGTATCAACTTTGTATGTGCACATGATGGAATTACACTCGCTGATTGGTAA	2220
2161	Db	CTTGGCACAGTATCAACTTTGTATGTGCACATGATGGAATTACACTCGCTGATTGGTAA	2220
2221	Qy	CATATAATAAGAAGTACAATTTACCAATGGGAGAAACAACAGAGATGGAGAAAAATCACA	2280
2221	Db	CATATAATAAGAAGTACAATTTACCAATGGGAGAAACAACAGAGATGGAGAAAAATCACA	2280
2281	Qy	ATCTTAGCTGGAATGTGGGAGGAAGAGAAATTCGCAAGATTGTCTGTCAAAAGATTGA	2340
2281	Db	ATCTTAGCTGGAATGTGGGAGGAAGAGAAATTCGCAAGATTGTCTGTCAAAAGATTGA	2340
2341	Qy	GGAAGGCGAGATCGCGAAATTTCTTGTTGTCTCATGTGTTTCTCAAGGAGTTCCTCAATGT	2400
2341	Db	GGAAGGCGAGATCGCGAAATTTCTTGTTGTCTCATGTGTTTCTCAAGGAGTTCCTCAATGT	2400
2401	Qy	TCTACATGGGTGATGAATATGGCCACAACAAGGGGGGCAACAACAATACATATCTGCCATG	2460
2401	Db	TCTACATGGGTGATGAATATGGCCACAACAAGGGGGGCAACAACAATACATATCTGCCATG	2460
2461	Qy	ATTCTTATGTCAATTATTCTTCGTGGGATATAAAAGAAACAATCTCTGAGTTGCACCGAT	2520
2461	Db	ATTCTTATGTCAATTATTCTTCGTGGGATATAAAAGAAACAATCTCTGAGTTGCACCGAT	2520
2521	Qy	CTTGCTGCCTCATGACCAAAATTCGCAAGGAGTGCAGGGTCTTTGGCCTTTGAGGACTTTC	2580
2521	Db	CTTGCTGCCTCATGACCAAAATTCGCAAGGAGTGCAGGGTCTTTGGCCTTTGAGGACTTTC	2580
2581	Qy	CAACGGCCAAACGGCTGCAGTGGCATGGTCTCAGCCTCGGAGCCCTGATTGCTCTGAGA	2640
2581	Db	CAACGGCCAAACGGCTGCAGTGGCATGGTCTCAGCCTCGGAGCCCTGATTGCTCTGAGA	2640
2641	Qy	ATAGCCGATTCGTTGCCCTTTTCCATGAAGATGAAGAAGGGCGAGATCTATGTGGCCT	2700
2641	Db	ATAGCCGATTCGTTGCCCTTTTCCATGAAGATGAAGAAGGGCGAGATCTATGTGGCCT	2700
2701	Qy	TCAACACCGCACTTACCGCGCTTGTTCAGCTCCAGAGCGGAGGCGCGGTGGG	2760
2701	Db	TCAACACCGCACTTACCGCGCTTGTTCAGCTCCAGAGCGGAGGCGCGGTGGG	2760
2761	Qy	AACCGGTGTGGACACAGGCAAGCCAGCACCATACGACTTTCCTCACGACGACTTACCTG	2820
2761	Db	AACCGGTGTGGACACAGGCAAGCCAGCACCATACGACTTTCCTCACGACGACTTACCTG	2820
2821	Qy	ATCGCGCTCTACGATACACAGTTCTCGGATTTCTCTACTCCAACTCTACCCCATGC	2880
2821	Db	ATCGCGCTCTACGATACACAGTTCTCGGATTTCTCTACTCCAACTCTACCCCATGC	2880
2881	Qy	TCAGCTACTCATCGGTTCATCTAGTATTTGGCCCTGATGTTTGAGAGACCAATATATACA	2940
2881	Db	TCAGCTACTCATCGGTTCATCTAGTATTTGGCCCTGATGTTTGAGAGACCAATATATACA	2940
2941	Qy	GTAATAATAATGTCTATGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2997
2941	Db	GTAATAATAATGTCTATGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2997

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; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT
; TITLE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
; FILE REFERENCE: 514413-3849.1
; CURRENT APPLICATION NUMBER: US/10/238,091
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: WO 99/58690
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: DE 198 20 608.9
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: 09/674,817
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Triticum aestivum L. cvFlorida
; US-10-238-091-2

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	Query Match	100.0%;	Score 2997;	DB 15;	Length 2997;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2997;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTCGGGGCGGCGCGCGCTCTGCGACGGTGGCAGCCCAATGCAGCGCGGGGAAGGGG	60		
Db	1	GTCGGGGCGGCGCGCGCTCTGCGACGGTGGCAGCCCAATGCAGCGCGGGGAAGGGG	60		
Qy	61	TCGGCGAGGTGTGGCGCGCGGTTCTCGAGGGCGCGACGAAGGTAGAGACGAGGGCGAGG	120		
Db	61	TCGGCGAGGTGTGGCGCGCGGTTCTCGAGGGCGCGACGAAGGTAGAGACGAGGGCGAGG	120		
Qy	121	AGGACGAGCGGTGGCGAGACAGGTACCGGCTCGGGCGCGGTGACGGGTGCTCGCGC	180		
Db	121	AGGACGAGCGGTGGCGAGACAGGTACCGGCTCGGGCGCGGTGACGGGTGCTCGCGC	180		
Qy	181	GAATGCCGCGCGCTGGGCGCACCGGCTCGCGGGGGGGTCAAATTCGCGCTCTATT	240		
Db	181	GAATGCCGCGCGCTGGGCGCACCGGCTCGCGGGGGGGTCAAATTCGCGCTCTATT	240		
Qy	241	CCGGCGAGCACACCGCGCGCGCTCTGCTCTTTCAGCCAGAAGATCTCAAAGCGGTGG	300		
Db	241	CCGGCGAGCACACCGCGCGCGCTCTGCTCTTTCAGCCAGAAGATCTCAAAGCGGTGG	300		
Qy	301	GGTTGCCCTCCGAGTAGAGTTTCATCAGCTTTGCGTGGCGCGCGCCCTTTTTTGGGCC	360		
Db	301	GGTTGCCCTCCGAGTAGAGTTTCATCAGCTTTGCGTGGCGCGCGCCCTTTTTTGGGCC	360		
Qy	361	TGCNATTTAGTTTTGTACTGGGCAAAATGCTGCAGATAGGGTGCACGAGAGTTCCC	420		
Db	361	TGCAATTTAAGTTTTGTACTGGGCAAAATGCTGCAGATAGGGTGCACGAGAGTTCCC	420		
Qy	421	CTTGACCCCTGATGAATCGGACCGGAAAGTGTGGCATGCTTCATCGAAGGCGAGCTG	480		
Db	421	CTTGACCCCTGATGAATCGGACCGGAAAGTGTGGCATGCTTCATCGAAGGCGAGCTG	480		
Qy	481	CACAACATGTTTACGGGTACAGTTTCGACGGCACCTTTGCTCCCTACTGCGGGCACTAC	540		
Db	481	CACNACATGTTTACGGGTACAGTTTCGACGGCACCTTTGCTCCCTACTGCGGGCACTAC	540		
Qy	541	CTTGAATGTTCCAAATGCTGGTGATTCCTTATGCTAAGCAGTGATGAAGCCGAGGGAG	600		
Db	541	CTTGAATGTTCCAAATGCTGGTGATTCCTTATGCTAAGCAGTGATGAAGCCGAGGGAG	600		
Qy	601	TATGGTGTTCGAGCGGTGTAAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT	660		
Db	601	TATGGTGTTCGAGCGGTGTAAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT	660		
Qy	661	CCATATAGCAGTTTGATTTGGGAAGGCGACTACTCTTAAGATATCTCTAAAGGACCTG	720		
Db	661	CCATATAGCAGTTTGATTTGGGAAGGCGACTACTCTTAAGATATCTCTAAAGGACCTG	720		
Qy	721	GTAATATATGAGATGCATTTGCGTGGATTCACGAAGCATGATTCAGCAATGTAGAACAT	780		

```

RESULT 2
US-10-238-091-2
; Sequence 2, Application US/10238091
; Publication No. US20030093834A1
; GENERAL INFORMATION:
; APPLICANT: Hoechst Schering AgrEvo GmbH
; APPLICANT: LSTR Horst
; APPLICANT: LETTICKE, Stephanie
; APPLICANT: ABEL, Gernot
; APPLICANT: GENSCHHEL, Ulrich

```


1564 GGATTTGCTGGTGGTTTGGCAATGCTTTTGTGGAGTCCACACCTATATACCAAGTAAGT 1623
1471 GGATTTGCTGGTGGTTTGGCAATGCTTTTGTGGAGTCCACACCTATATAC 1521
1624 TGTGGCAATACTTGTAAATGAGTTGAGTGAATGTCACCTGGATTTTATATATACCA 1683
1522 ----- 1521
1684 TGATGATACACATCTAAATATATAACAATCATAGTGTATGATATGCAATTTGGCTAAGAA 1743
1522 ----- 1521
1744 GTATTAGTGTATACACTAGTGTATATATATAGGTTTAAACCCAACTTGCCAAATGAAGAA 1803
1522 ----- 1521
1804 ACATAGGCTTTCTAGTTAATCTTATTTATTTGTCGGTGAATAATCCACTGAAATAATCC 1863
1522 ----- 1521
1864 AGCCATGTCATTTTATAGGGGGGAGAGAAACTATATTTGATTTGCCCCCTAAAGAAAG 1923
1522 ----- 1521
1924 CCATCTCAGAATTCATAGGTAAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCATATCT 1983
1522 ----- 1521
1984 TTCTATCGGTCTAACTTAGCTCGATGTATATTTGTAAGATGAATGCCAAATTTAATTTG 2043
1522 ----- 1521
2044 TCGGATAATTTGATCTGTTATTCACAAATTTCTATTGTTTCTTAGAAATCCAAACAG 2103
1522 ----- 1521
2104 TAACTTGTATTGCACTGCACTTCTTATTGATTAATCAGGAGGAGGAGGAAACCTT 2163
1522 ----- 1521
2164 GGCACAGTATCACTTTGTATGTGCATGATGATGATTTACCTGGCTGATTTGGTAACAT 2223
1544 GGCACAGTATCACTTTGTATGTGCACACGATGATTTACCTGGCTGATTTGGTAACAT 1603
2224 ATATAGAGAGTCAATTTTACCAATCGGGAGAACACAGAGATGAGAGAAATCACAATC 2283
1504 ATATACAGTACATTTTACCAATCGGGAGAACACAGAGATGAGAGAAATCACAATC 1663
2284 TTAGCTGGAAATTTGGGGAGGAGGAGAAATTCGCAAGATTTGCTGCAAAAGATTGAGGA 2343
1664 TTAGCTGGAAATTTGGGGAGGAGGAGAAATTCGCAAGATTTGCTGCAAAAGATTGAGGA 1723
2344 AGAGCAGATGCGCAATTTCTTTGTTGCTCTCATGTTTCTCAGAGATTCGAATGTTCT 2403
1724 AGAGCAGATGCGCAATTTCTTTGTTGCTCTCATGTTTCTCAGAGATTCGAATGTTCT 1783
2404 ACATGGTGTATGATATGGCCACACAAAAGGGGCAACAAATACATATCTGCAATGAT 2463
1784 ACATGGTGTATGATATGGCCACACAAAAGGGGCAACAAATACATATCTGCAATGAT 1843
2464 CTTATGTCATATTTTCGGTGGGATAAAGAAACAAATCTGATGTTGCACCGATTTCT 2523
1844 CTTATGTCATATTTTCGGTGGGATAAAGAAACAAATCTGATGTTGCACCGATTTCT 1903
2524 GCTGCTCATGACCAAAATTCGCAAGGAGTGGAGGCTTTGCGCTTGAGGACTTTCCAA 2583
1904 GTTGCCTCATGACCAAAATTCGCAAGGAGTGGAGGCTTTGCGCTTGAGGACTTTCCAA 1963
2584 CGGCCAAACGGCTGCACTGATGATGATCAGCTGCGGAGAGCTGATTTGGTCTGAGAAATA 2643
1964 CGGCCAAACGGCTGCACTGATGATGATCAGCTGCGGAGAGCTGATTTGGTCTGAGAAATA 2023
2644 GCGGATTCGTTGCTTTTCCATGAAGATCAAGACAGGCGGAGATCTATGTCGCTTCA 2703

2024 GCCGATTCGTTGCTTTTCCATGAAGATGAAGACAGGGCGAGATCTATGTGCTTCA 2083
2704 ACACGAGCACTTACCGGCGCTTTGAGCTCCAGAGCGCGAGGGCGCGGTGGGAAC 2763
2084 ACACGAGCACTTACCGGCGCTTTGAGCTCCGAGGCGCACAGGGCGCGGTGGGAAC 2143
2764 CGGTGGTGGACACAGGCAAGCCAGACATACGACTTCTCTCACGAGACTTACCTGATC 2823
2144 CGGTGGTGGACACAGGCAAGCCAGACATACGACTTCTCTCACGAGACTTACCTGATC 2203
2824 GCGCTCTACCATACACAGTTCTCGGATTTCTCTACTTCCAACTCTACCCCATGCTCA 2883
2204 GCGCTCTACCATACACAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2263
2884 GCTACTCATCGTCTCATCTCTAGTATTGCGCCCTCTAGTATTGAGACCAATATATACAGTA 2943
2264 GCTACTCATCGTCTCATCTCTAGTATTGCGCCCTCTAGTATTGAGAGGC--GGATATACAGTA 2321
2944 AATAATATGCTATATGTA 2962
2322 AATAATATGATATATGTA 2340

RESULT 4
US-10-437-963-88689
; Sequence 88689, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88689
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87515C.1
US-10-437-963-88689

Query Match 36.2%; Score 1085.2; DB 17; Length 2307;
Best Local Similarity 67.7%; Pred. No. 8.7e-285;
Matches 1924; Conservative 0; Mismatches 273; Indels 645; Gaps 3;

120 GAGCAAGAGCGGTGGCGGAGGACAGGTACGCTCGCGCGCGGTGCGAGGTGCTCGCC 179
1 GTGAGGCGGTGGTGTATCGCGAGAGGTACGCGTGGGTGGCGGTGCGAGGTGCTCGCC 60
180 GGAATGCCCGCGCGCTGGGCGCCACCGCTCGCGCGCGGTCAATTTCCCGCTCTAT 239
61 GGAATGCCCGCGCGCTGGGCGCCACCGCTCGCGCGCGGTCAATTTCCCGCTCTAC 120
240 TCCGCGGAGCACCGCGCGCGCTCTGCTCTTCTACGCGAGAGATCTCAAGCGGTG 299
121 TCCGCGGCGCATCGCGCGGTGCTCTGCTCTTACCCCGCGAGATCTCGAGGC--- 176
300 GGGTGTCTCCGAGTAGAGTTCAATGCTTGGTGGCGCGCGCCCTTTTGGGC 359
177 ----- 176
360 CTGCAATTTAAGTTTGTGTCTGGGGCAATGCTGACAGATAGGTGACCGAGGAGTTCC 419

QY 1396 ATTGACATGATCAGCAATGACCCAAATCTTTGGAGGCGTCAAGCTCATTTGCTGAAGCATGG 1455
Db 1484 ATTGACATGATGACCAATGACCCAAATCTTTGGAAATGTCGAAGCTCATTTGCTGAAGCATGG 1543
QY 1456 GATGCGAGGAGCTCTATCATAGTAGTCAATTCCTCCTCAGTGAATCTTTGCTGAGTGG 1515
Db 1544 GATGCGAGGAGCTCTATCATAGTAGTCAATTCCTCCTCAGTGAATCTTTGCTGAGTGG 1603
QY 1516 AATGGGAAGTACCGGGACATTTGCGCTCAATTCATTAAAGGCACTGATGATTTGCTGGT 1575
Db 1604 AATGGGAAGTACCGGGACATTTGCGCTCAATTCATTAAAGGCACTGATGATTTGCTGGT 1663
QY 1576 GATTTTGGCCCAATGCTCTTCTGGAAGTCCACACCTATACAGTAAAGTTTGCCATATCT 1635
Db 1664 GCATTTGCTCAATGCTCTATGGAAGTCCACAGTTATAC 1702
QY 1636 TGTAATAGTGTGAGTGAATGTCACTGGGATTTTTATATATACCATGATGATACACA 1695
Db 1703 ----- 1702
QY 1696 TCTAAATATATAAATCATAGTGTATGATATGCAATTTGGCTAAGAATATTAGTGTAT 1755
Db 1703 ----- 1702
QY 1756 ACTAGTGTATATATAGTGTATTAACACCCAACTTGCCAAATGAAGAAACATAGGCTTT 1815
Db 1703 ----- 1702
QY 1816 CTAGTTATCTTATTTATTTGCGGTGAATTAATCCACTGAAATTTCCAGCCATGCAAT 1875
Db 1703 ----- 1702
QY 1876 TTTTAGGGGGAGAGAACTATATTGATTTGCCCCCTTAAAGAGCATCTCAGAAAT 1935
Db 1703 ----- 1702
QY 1936 TCATAGTAAAGTTGCTTTCTGTAAAGAAAGAAACGACTTCATCTTTCTATCGGTGC 1995
Db 1703 ----- 1702
QY 1996 TAACCTAGCTGATGATATTTGTAAGATGAATGCCAAATTTAATTTGTCGGATATTTG 2055
Db 1703 ----- 1702
QY 2056 ATCTGTATTACAAATTTCTATTGTTGTTCTCTAGAAATCAAAACGATTAATTTGTTAT 2115
Db 1703 ----- 1702
QY 2116 GGCACCTGCACTTTTATGATTAATCAGCAGAGAGAGAAACCTTTGGCAAGTATCA 2175
Db 1703 -----CAGCAGGGGGAGAGAAAGCCTTTGGCAAGTATCA 1736
QY 2176 ACTTTGATGTGCATGATGGATTTTACACTGGCTGATTTGGTAAACATATAAAGAAGT 2235
Db 1737 ACTTTGATGTGCATGATGGATTTTACACTGGCTGATTTGGTAAACATATAAAGAAGT 1796
QY 2236 ACAATTTACCAATTTGGGAGAACACAGAGATGGAGAAATTCACATTTTAGCTGGAAT 2295
Db 1797 ACACTTGTCAATTTGGTGAGCAACAGAGATGGGAAATTCATATCTTAGCTGGAAT 1856
QY 2296 GTGGGAGGAGAGATTCGACAGATTTCTGTCAAAAGATTCAGAGAGAGAGATGC 2355
Db 1857 GTGGGAGGAGAGATTTGCAAGTCTGTCTGAGTCCGAAGATTAAGAGAGAGCAATGC 1916
QY 2356 GCAATTTCTTTGTTGCTCATGTTTCTCAAGGAGTTCCAAATGTTCTACATGGGTGATG 2415
Db 1917 GCAATTTCTTTGTTGCTCATGTTTCTCAAGGAGTTCCAAATGTTCTACATGGGTGATG 1976
QY 2416 AATATGGCCACAAAAAGGGGGCAACAAATACATCTGCCATGATTTCTTATGTCAT 2475
Db 1977 AATATGTCACAAAGGGGGCAACAAATACATCTGCCATGATTTCTTATGTCAT 2036
QY 2476 ATTTTCGCTGGGATAAAA---AAGAACAACTCTCTGATTTGACCGGATTTCTGCTGCCTCA 2532

Db 2037 ATTTCCGTTGGATTAAGAAAGAAACAAATCTCTGATTTGTACAGATTTCTGCGGTCTCA 2096
QY 2533 TGACCAAAATTCGCAAGAGTGCAGAGGCTCTTGGCTTTGAGGACTTTTCCAAACGGCAAC 2592
Db 2097 TGACCAAAATTCGCAAGAAATGTGAATCTCTTGGCTTTGAGGACTTTCCGACTTCAGAAC 2156
QY 2593 GGCTCAATGGCATGCTCATCAGCCTTGGAAAGCCTGATTTGCTGAGAAATAGCCGATTCG 2652
Db 2157 GGTGAAATGTCAGCGTTCATCAGCCCGGAAAGCCTGATTTGCTGAGGCAAGCCGATTCG 2216
QY 2653 TTGCTTTTTCATGAAGATGAAGACAGGCGGAGATCTATGTGGCTTTCAACACCCAGCC 2712
Db 2217 TTGCTTTTTCATGAAGACAGGCGGAGATCTATGTGGCTTTCAACACCCAGCTC 2276
QY 2713 ACTTACCGGCGCTTTTGAAGTCCAGAGCGCGGAGGCGCGGTGGGAAACGCTGGTGG 2772
Db 2277 ACCTTCCGTTGGTGTGTTGGGCTTCCAGAGCGCTCTGGGTTCCGATGGGAGCGGTTGGTGG 2336
QY 2773 ACACAGGCAAGCCAGCACCATACGACTTCCCTCACCAGAGCTTACCTGATCGGCTCTCA 2832
Db 2337 ACACGCGCAAGGAGGACCATATGACTTCCCTACCGATGGGCTGCCAGATCGTCTGTCA 2396
QY 2833 CCATACACAGTTCCTCGCATTTCTCTACTCCAACTCTACCCCATGCTCAGTACTCAT 2892
Db 2397 CGGTCTACAGTTCTCTCTATTTCTCTCACTCAATCTCTATCTATGCTCAGTACTCT 2456
QY 2893 CGGTCTCTAGTATTTGGGCTGATTTGTGAGAGACCAATATATA 2938
Db 2457 CCATCATCTTTGATTTGGGCTGATTTGTGAGAGACCAATATATA 2502

RESULT 6
US-10-425-114-19788
; Sequence 19788, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19788
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-045;C7_FLI
US-10-425-114-19788

Query Match 25.9%; Score 777; DB 13; Length 1866;
Best Local Similarity 65.4%; Pred. No. 1.1e-200;
Matches 1477; Conservative 0; Mismatches 250; Indels 530; Gaps 2;
QY 685 GCGGACCTTACCTTAAGATATCTCCTCAAGAGCCTGGTAATATATATAGATGACACTTGGT 744
Db 1 GGTGACCTTACCTTGGGTACCATCAGAGGACCTTGTCTATATATGAATGCAATTTGGCT 60
QY 745 GGATTCAGCAAGCATGATTCAAGCAATGTAGAACAATCCGGGTACTTTTCATTGGAGCTGTG 804
Db 61 GGATTCACAAAGCACAACTCAAGCAAGACAAACACCCAGGAACCTTACATTGGTGTGTG 120
QY 805 TCGAGCTTGAATTTGAAGAGCTTGGAGTAAATTTGATTTGAATTAATGCCCTGCCAT 864
Db 121 TCAAGGCTTGACCATCTAAAGGAACTTGGAGTGAATCTGTAGAGCTAATGCCCTGCCAT 180

QY 865 GAGTCAACGAGCTGGAGTACTCAACCTCTCTTCCAGATGAACCTTTGGGGATATCT 924
DB 181 GAGTCAATGAGCTAGAGTACTTCAGCTCTCTTCCAGATGAACCTTTGGGGATATCT 240
QY 925 ACCATAACTCTTTTCCACCAATGACAGATACACATCAGCGGGATNAACACTGTGG 984
DB 241 ACAATAAATTTTTCTCACCAGATGGCAAGATATCTTCAAGTGGCATAAGAGACTCTGGA 300
QY 985 CGTGATGCCATAATGAGTTCAAACTTTTGAAGAGAGCTCACAAACGGGAAATGAG 1044
DB 301 TGTGGTCCCATAAATGAATTAAGCTTTTGAAGGAGGCCACAAACGGGAAATGAG 360
QY 1045 GTGATCTGATGTGTCTTCAACCATACAGCTGAGGGTAATGAGAAATGCTCAATATTA 1104
DB 361 GTGATCATGATGTGTCTTCAATCATACAGCTGAAGGTAAAGAGAAAGGCCCAATATTA 420
QY 1105 TCATTAAAGGGTGGATAATCTACATATATATGCTTGCACCTAAGGGAGAGTTTAT 1164
DB 421 TCCTTAAAGGGGATAGATAATAGTACATATATGCTTGCACCTAAGGGAGAGTTTAT 480
QY 1165 AACTATCTGCTGGGATATACCTTCACTGTAATCATCTGTGTGCTCAATTCATT 1224
DB 481 AATTATTTCTGTTGGAAATACCTTCAATGTAATCATCTGTGTGCTCAATTCATT 540
QY 1225 GTGATTTGTTAGATCTGGTGAAGAAATGCAATGCTGATGCTGTTGCTTTGATCTT 1284
DB 541 GTGATTTGTTAGATCTGGTGAAGAAATGCAATGCTGATGCTGTTGCTTTGACCTT 600
QY 1285 GCATPCCATATGACAGAGTTCAGTCTGTGGATCCAGTTAACTGATGAGCTCCA 1344
DB 601 GCATPCCATATGACAGAGTTCAGTCTGTGGATCCAGTTAACTGATGAGCTCCA 660
QY 1345 ATAGAAGTGCATGATCAACAGGAGACCTCTTGTACTCCACACTTATGACATG 1404
DB 661 ATGAAGGTGACATGATGACAGAGGACCTCTTGTGCCCCACCACTTATGACATG 720
QY 1405 ATCAGCAATGACCAATCTTGGAGGCTCAAGCTCATTTGCTGAAGCTGGATGACGA 1464
DB 721 ATTAGCAATGACCAATCTTGGAGGCTCAAGCTCATTTGCTGAAGCTGGATGACGA 780
QY 1465 GGCTCTATCAAGTGTCAATTCCTCTCACTGGAATGTTTGGTCTGAGTGGAAATGGAAG 1524
DB 781 GGTCTCTATCAAGTGTGCTAGTTCTCTCACTGGAACGTTTGGTCAAGTGGAAATGGAAG 840
QY 1525 TACGGGACATTTGGCTCAATTCATTAAGGCACTGATGATTTCTGCTGCTTTTGGC 1584
DB 841 TATCGCATACCGTGTGCTAGTTCTCACTGGAACGTTTGGTCAAGTGGAAATGGAAG 900
QY 1585 GAATGCTTTTGTGAAGTCCACACTTATACAGGTAAGTTGTGGCAATCTTGTAAATGA 1644
DB 901 GAATGCTTTTGTGAAGTCCACAGTTATAC----- 930
QY 1645 GTTGAGTGTACCTGGATTTTATATATACCACATGATACACATCTAAATAT 1704
DB 931 ----- 930
QY 1705 ATAACAATAGTGTATGATATGATTTGGCTAAGAAATATAGTGTATACACTAGTG 1764
DB 931 ----- 930
QY 1765 CTATATAGGTTTAAACCCAACTTGGCAATGGAAGAACATAGGGCTTTCTAGTTATC 1824
DB 931 ----- 930
QY 1825 TTATTTATTTGTCGGTGAATAATCCACTGAAAAATTCAGCCATGTCATTTTATGGGG 1884
DB 931 ----- 930
QY 1885 GGGAGAGAACTATATGATTTGGCCCCCTAAAGAGCCATCTCAGAAATCATAGGTA 1944
DB 931 ----- 930
QY 1945 AGTTGCTTTTCTGTAAGAGAAAGAAACGACTTCATACCTTTCTATCGGTCTAACTTAGC 2004

DB 931 ----- 930
QY 2005 TCGATGTATATTTGTAGATGAATGTCACAAATTTAATTTGTCGGATAAATTTGATCTGTAT 2064
DB 931 ----- 930
QY 2065 TCACAAATTTCTATTTGGTTTCTCTAGAAATCAAAACAGTAACCTTTATTTGGCACTGCA 2124
DB 931 ----- 930
QY 2125 ACTTCTTATTAATTAATCAGCGAGGAGAGAAACCTTTGSCACAGTATCAACTTTGTAT 2184
DB 931 -----CAGCGAGGGGAGAGAAACCTTTGSCACAGTATCAACTTTGTAT 973
QY 2185 GTGCACATGATGATTTTACACTGGCTGATTTTGGTAAACATATAATAAGAAAGTACAATTTAC 2244
DB 974 GTGCACACGATGATTTTACACTGGCTGATTTTGGTCAACATACATAGCAAGTACAACCTGT 1033
QY 2245 CAATGGGGAGAAACACAGAGATGAGAAATCAATCTTTAGCTGGAATTTGGGAGG 2304
DB 1034 CAATGGGTGAGGACACAGAGATGGGAAATCATNAATCTTTAGCTGGAATTTGGGAGG 1093
QY 2305 AAGGAGAAATTCGCAAGATTTGCTCAAAAGATTTGAGAGAGGACAGATGGCAATTTCT 2364
DB 1094 AAGGAGAAATTTGCAAGTCTGTCAGTCCGAAGATTTAAGAGAGGCAATTTGGCAATTTCT 1153
QY 2365 TTGTTTGTCTCATGTTTCTCAAGAGTTTCAATGTTCTCATGGGTGATGAATATGGCC 2424
DB 1154 TTGTTTGTCTCATGTTTCTCAGGAGTTTCAATGTTCTCATGGGTGATGAATATGGTC 1213
QY 2425 ACACAAAGGGGGCAACAAATACATCTGCAATGATTTCTTATGTCAATTTATTTTCGT 2484
DB 1214 ACACAAAGGGAGGACAAACATAGTCTGCAATGATGACCAATATGTCAATTTATTTCCGT 1273
QY 2485 GGGATAAAA---AAGAACAAATCTCTGAGTTGCAACCGATTTGCTGCTCATGACCAAT 2541
DB 1274 GGGATAAAGAGAAACAAATCTCTGATTTGTACAGATTTGCGCTCTCATGACCGAAT 1333
QY 2542 TCCGCAAGAGTGGAGGGTCTTGGCTTGAGGACTTTCCAAAGCCCAAGCGCTGCAGT 2601
DB 1334 TCCGCAAGAAATGTGAATCTCTTGGCTTGAGGACTTTCCGACTTCAGAACGGTTGAAAT 1393
QY 2602 GGCATGTGCTACAGCTTCCGGAAGCTGATTTGGTCTGAGAAATAGCCGATTTGCTTTCCTTTT 2661
DB 1394 GGCAGGTCTACAGCCCGGGAAGCTTACCTGGTCAGAGGCAAGCCGATTCGTTGCCCTTCA 1453
QY 2662 CCATGAAGATGAAAGACAGGGCGAGATCTATGTGGCTTCAACACAGGCCACTTACCGG 2721
DB 1454 CCATGAAGGACGAAACCAAGGCGAGATCTACGTGGCTTCAACACAGCTCACCTTCCGG 1513
QY 2722 CCGTTGTTGAGCTCCAGAGCGCGAGGGCTGGGAACCGGTGGTGGTGGTGGACACAGGCA 2781
DB 1514 TGGTTGTTGGCTTCCAGAGCGCTCTGGTTCGATGGGAGCGGTGGTGGTGGACACAGGCA 1573
QY 2782 AGCCAGCACCATACAGCTTCTCACCAGCACTTACCTGATGCGGCTCTCACCATACACC 2841
DB 1574 AGGAGGACCATATGATCTTCTCACCAGTGGCTTCCAGATCGGTGCTGCTCACCGTCTACC 1633
QY 2842 AGTTCTCGCATTTCTCTACTCCAACTCTACCCACTGCTCAGCTACTCTCGTCTATCC 2901
DB 1634 AGTTCTCTCATTTCTCACTCCAACTCTATCTCTATGCTGCTGCTGCTGCTGCTGCTGCT 1693
QY 2902 TAGTATTTGGCCCTGATTTTGAAGACCAATATATA 2938
DB 1694 TTGATTTGGCCCTGATGTTCTGAAAGAGCAGATACA 1730

RESULT 7

US-09-938-842A-218
; Sequence 218, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 218

LENGTH: 2352

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-218

Query Match 22.0%; Score 658.4; DB 9; Length 2352;

Best Local Similarity 71.2%; Pred. No. 3.3e-168;

Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

389 TGCTGACGATAGGTCACCGAGGAGTTCCTTGCACCCCTGATCGAATCGGACCGGA 448

323 TCCGTGACAAAGTACCGAGAGATTCAGCTTGATCCATCAAGAAATAGAACTGGCC 382

449 ACCTGTGGCATGCTTCATCGAAGCGAGCTGCACACATGCTTTACGGGTACAGGTTG 508

383 ATGTTTGGCATGTTCTTGGAGGAGATTTCAAAGATATGTTGATGTTATAGATTG 442

509 ACGGACCTTTGCTCCTCACTGCGGGGACCTACCTTGATGTTTCAATGTCGTGGTGCATC 568

443 ATGGCAAGTTTCTCCTCGAAGAGGTCATTTATGATTCCTCCAACTTTTATTTGGATC 502

569 CTATGCTAAGGACGATGATTAAGCGAGGAGTATGTTTCCAGCGCGTGTAAACAAT 628

503 CTACGCAAGGCAATTAAGCAGAGATGATGTTTGGAGTTTGGACCTGATGATTAAT 562

629 GCTGCTCATAGGCTGGCATGATCCCTCTTCCATATAGACGTTTGTATGGAAGGCG 688

563 GTTGGCTCAATGGCTGTATGTACCCACTCGTAGGAAGAGTTTGTATGGAAGGCG 622

689 ACCTACCTTAAGATATCCTCAAGACCTGGTAAATATATAGATGACCTTCGCTGGAT 748

623 ATATGCACTGAAGCTTCCACAGAAATCTTGTATATGAAATGCATGTCGAGGTT 682

749 TCAGCAAGCATGATTCAGCAATGTAGAACATCCGGGTACTTTCAATGGAGCTGTGTGCA 808

683 TTCAAGGACATGATCTAGTAAATTCATTCCTGSCACATACCAGGGTGTTCAGAGA 742

809 AGCTTGACTATTGAAGGAGCTTGGAGTTAATGTTATGTAATTAATGCTGCTGATGAT 868

743 AGCTTGACCAATTTGAAGGAGCTTGGGATAAATGTATAGAATTAATGCCATGTCCAGAT 802

869 TCAAGGAGCTGGAGTACTCAACCTCTTCTTC-----CAAGATCAACTTTT 913

803 TTATGAGCTGGAGTATTACAGCTACATAGGATTTGGAGACCAAGGTTAAATTTT 862

914 GGGGATATTTCATAAATCTTTTTCACCAATGACAAATGACATACATAGGCGGATAA 973

863 GGGGTACTCTACCAATTTGGTCTCTCTCGCCATGATCAGATACGATCAGCAAGCTCTA 922

974 AAACTGTGGCGTGGATGCTTAATGATGTTTCAAACTTTTGTAAAGAGGCTTCACAAAC 1033

923 ACAATTTGCTGGAGGAGCCATAAATGAATGAAATTTCTTTTAAAGAGGACATTAAC 982

1034 GGGGAATGAGGTGATCTGATGATTTGTTCTTCAACCATACAGCTGAGGGTAAATGAGATG 1093

983 GAGGAATGAGTAATCATGATGCTGCTTTTGAACCAACACAGCGGAAGGAATGAAAG 1042

1094 GTCCAAATATTATCATTTAAAGGGGTCGATAATACTATACATATATATGTTGACCCAAAG 1153

1043 GGGCCATTTTCTCATTTAGAGGAGTTGATAACAGAGTGTCTATTACATGTTGCTCCAAAG 1102

1154 GAGGTTTTTAACACTATTCTGCTGGGAATACCTTCAACTGTAATCATCTCTGTGGTTC 1213

1103 GGGGTTCTTAATATTATTCAGGCTGTGTAATAATCATCACTGCAATCATCTGTGGTTC 1162

1214 GTCAATTCATTGTAGATTGTTTAAAGATACTCGGTGACGGAATGATGTTGATGTTTTC 1273

1163 GTCAATTCATTGTAGATTGTTTAAAGATACTCGGTGACGGAATGATGTTGATGTTTTC 1222

1274 GTTTTGTATCTTGCATCCATAATGACAGAGTTCCAGTCTGTGGATCCAGTTAACGTT 1333

1223 GCTTTGATCTTGGTTCAATCATGTCAAGAGCAGCAGCTTTGGATCCAGCAATGTTT 1282

1334 ATGAGAGCTCCAAATAGAGGTGACATGATCAACAAGGACACCTCTTCTTACTCCACCAC 1393

1283 ACGGGGCTGATGTAGAGGTGACTTGTCTCAACACTGGTACTCTTATTAGTGCCTCCAG 1342

1394 TTATTTGACATGATCAGCAATGACCAATCTTGGAGGCTCAAGCTCATCTGTAAGCAT 1453

1343 TAAATGACATGATAAGTAATGATCCATCTCCGCGTGTAAAGTAATAGCTGAAGCAT 1402

1454 GGGATGACAGGAGGCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGT 1513

1403 GGGATGACAGGAGGCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGT 1462

1514 GGAATGGAAAGTACCGGACATTTGCGTCAATTCATTTAAAGGCACTCATGATGATTTGCTG 1573

1463 GGAATGGAAAGTACCGGACATTTGCGGATGTTGAGACAGTTTCAAAAAGGCACTGATGCTG 1522

1574 GTGGTTTTGCGAAGTCTTTGTGGAAGTCCACACCTATACAGGTAAGTTG 1625

1523 GTGCTTTGCTGATGTTCTGTGGAAGCCCAATCTGTACAGGAGGTAG 1574

RESULT 8

US-09-938-842A-218

Sequence 218, Application US/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 218

LENGTH: 2352

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-218

Query Match 22.0%; Score 658.4; DB 11; Length 2352;

Best Local Similarity 71.2%; Pred. No. 3.3e-168;

Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

389 TGCTGACGATAGGTCACCGAGGAGTTCCTTGCACCCCTGATCGAATCGGACCGGA 448

323 TCCGTGACAAAGTACCGAGAGATTCAGCTTGATCCATCAAGGAATAGAACTGCC 382

QY 449 ACGTGTGGCTGCTTTCATCGAAGCGAGCTGCACAAATGCTTTAGCGGTACAGGTTG 508
Db 383 ATGTTTGGCTGCTTCTTGAGAGGAGATTCAAAGATATGTTGATAGATTG 442
QY 509 ACGGCACTTGTCTCCTCACTGCGGCACTACCTTGATGTTTCAATGTCGTGATG 568
Db 443 ATGGCAAGTTTCTCCCTGAAGAAGGTCATTATTATGATTCCTCCAAATTTTATTGATC 502
QY 569 CTTATGCTAAGCGAGTGCATTAAGCGGAGGAGTATGTTTCCAGCGCGTGTAAACAATT 628
Db 503 CTTACGCAAGGCAATTAATAGCAGAGATGATGTTTGGAGCTGATGATTAAT 562
QY 629 GCTGGCTCAGATGCTGCGCATGATCCCTCTTCATATACAGCATGTTGATGGAAGGCG 688
Db 563 GTTGGCTCAAAATGGCTGTATGTTACCCACTCGTGAGGAAGAGTTTGTATGGGAAGGG 622
QY 689 ACCTACCTCTAAGATATCCTCAAAAGGACCTGTTATATATATGATGATGCACTTCGCTGAT 748
Db 623 ATATGCACTGAAGCTTCCACAGAAAGATCTTGTATATATGAAATGCAATGCGAGGTT 682
QY 749 TCACGAAGCATGATTAAGCAATGTAGAACATCGGCTACTTTCAATGGAGCTGTGCGA 808
Db 683 TTACAGGCACTGACTAGTAAATAATGAAATCCCTGGCACATACCAAGGTTGTCAGAGA 742
QY 809 AGCTTGACTATTGAAGGAGCTGGAGTTAATGTTATGTAATTAATGCCCTGCCATGAT 868
Db 743 AGCTTGACCAATTTGAAGGAGCTGGGATAAATTTATAGAAATTAATGCCATGTCAGAGT 802
QY 869 TCACGAGCTGGAGTACTCAACTCTCTCTTC-----CAAGATGAACCTTT 913
Db 803 TTAATGAGCTGGAGTATTACAGCTACATACGATTTTGGGAGACACAGGTAATTTT 862
QY 914 GGGGATATTACATTAATCTTTTTCACCAATGACAGATACACATCAGCGGCGGATTA 973
Db 863 GGGGTACTCTACCAATTTGGTCTTCTCGCCCATGATCAGATACGATCAGCAAGCTCTA 922
QY 974 AAAAAGCTGGCGGTGATGACATAATGAGTTCAAACTTTTGAAGAGAGGCTCAAAAC 1033
Db 923 ACATTTTGTGGAGAGACCAATAATGAATTCAAATTTTGAAGAGGACATTAAC 982
QY 1034 GGGGATTTGAGTGTATCTGATGTTGTTCTTCAACCATACAGCTGAGGTAATGAGAAATG 1093
Db 983 GAGGAATTTGAGTAATCATGATGCTGTTCTTGAACCAACAGCGGAGGGAATGAAGAAAG 1042
QY 1094 GTCCAAATATTATCAATTAAGGGGTGATAATACATACATATATGCTTGACCCCAAG 1153
Db 1043 GGGCCATTTCTCATTTAGAGGAGTTGATAACAGTGTCTATTACATGCTTGTCTCAAGG 1102
QY 1154 GAGAGTTTATACTATTCTGGCTGGGAATACCTTCAACTGTAATCATCTCTGTGGTTC 1213
Db 1103 GCGAGTTCTATAATTTATGAGGCTGTGTAATACATTTCAACTCAATCATCTCTGTGTCG 1162
QY 1214 GTCAATTCATGATGATGTTTGAAGTACTGGGTGACGGAATGCAATGATGATGTTTC 1273
Db 1163 GTCAATTCATGATGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222
QY 1274 GTTTTGTATCTTGATCATTAATACAGAGGTTTCCAGTCTGTGGGATCCAGTTAAGCTGT 1333
Db 1223 GCTTGTATCTTGTTCATCTCATGTCAAGGAGCAGCAGCTTTGGGATGAGCCATGTTT 1282
QY 1334 ATGGAGCTCAATAGAGAGGTGACATGATCAACAGGGAACCTCTTGTATCTCCACAC 1393
Db 1283 ACGGGCTGATGATGAGAGGTGACTTGTCTCAAACTGCTACTTCTATAGCTGCTCCAG 1342
QY 1394 TTATTGATCATGATCAGCAATGACCAATCTTGGAGCGTCAAGCTCATTTGCTGAAGCAT 1453
Db 1343 TAATTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1402
QY 1454 GGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTTGGTCTGAT 1513
Db 1403 GGGATGAGGCTGCTGATCAAGTGTGGATGTTTCCACACTGGGTAATTTGGTCTGAT 1462
QY 1514 GGAATGGGAAGTACCGGACATTTGTGCTCAATTTCAATTAAGGCACTGATGGATTTGCTG 1573

Db 1463 GGAATGGAAGTTTCGGGATGTTGTGAGACAGTTTCATAAAGGACCGATGGCTTTTCTG 1522
QY 1574 GTGGTTTTCGGAATGCTTTGTGGAAGTCCACACCTATACCAAGTAAAGTTG 1625
Db 1523 GTGCTTTTGTGGAATGCTCTGTGGAAGCCCAAAATCTGTACCAAGGAGTAG 1574

RESULT 9
US-10-425-114-20367
; Sequence 20367, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20367
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3180-047-B3_FLI
US-10-425-114-20367

Query Match 19.8%; Score 594.2; DB 13; Length 1198;
Best Local Similarity 84.4%; Pred. No. 6.8e-151;
Matches 681; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
QY 2135 GATTAATCAGGACAGGAGGAGAAACCTTGCCACAGATCAACTTCTGATGTCACATGA 2194
Db 205 GTTATACAGGACAGGAGGAGAGCCCTTGGCACAGTATCACTTGTATGTCACACGA 264
QY 2195 TGGATTTACACTGGCTGATTTGGTAAACATATAATGAAGTACAAATTTACAAATGGGA 2254
Db 265 TGGATTTACACTGGCTGATTTGGTAAACATATAATGAAGTACAACTTGTCAAATGGTA 324
QY 2255 GAAACAAGAGATGGAGAAATCAATCTTAGCTGGAATTTGGGAGGAGAGAAAT 2314
Db 325 GGACAACAGAGATGGGAAATCAATCTTAGCTGGAATTTGGGAGGAGAGAAAT 384
QY 2315 CGCAAGATTTCTGTCAAAAGATTGAGGAAGAGCAGATCGCAATTTCTTTGTTGCT 2374
Db 385 TGCAAGTCTGTCTGCGAAGATTAAAGAGAGCAGCAATTTGCGCAATTTCTTTGTTGCT 444
QY 2375 CATGGTTTCAAGAGGTTCCAAATGTTCTACATGGGTGATGAATATGCGCACACAAAGG 2434
Db 445 TATGGTTTCTCAGGAGTTCCAAATGTTCTACATGGGCGATGAATATGTCACAAAGG 504
QY 2435 GGGCAACAACAAATACATCTAGCTGCAATTTCTTATGTCAAATTTTTCCTGGGATAAAA - 2493
Db 505 AGGGAACAACAAATACATCTAGCTGCAATTTCTTATGTCAAATTTTTCCTGGGATAAAA 564
QY 2494 --AAGAACAAATCTCTGAGTTGACACCAATTTCTGCTGCTCATGACCAAAATTCGCAAGGA 2551
Db 565 GGAAGAACAAATCTCTGAGTTGACACCAATTTCTGCTGCTCATGACCAAAATTCGCAAGGA 624
QY 2552 GTGCGAGGCTCTGCGCTTGGAGGACTTTCCAAAGCCCAACCGCTGCGAGTGGCATGCTCA 2611
Db 625 ATGTAATCTCTTGGCTTTGAGGACTTCCGCACTTCAGAACGGTTGAAATGGCAGCGTCA 684
QY 2612 TCAGCTCTGGGAAGCTGATTTGGTCTGAGAAATAGCCGATTCGTTGCCCTTTTCCATGAAGA 2671
Db 685 TCAGCCCGGAAGCTGACTGCTGAGAGGAGCAAGCCGATTCGTTGCCCTTTCACCATGAAGA 744

APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(531313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6193
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700556474_FLI
US-10-425-114-6193

Query Match 14.0%; Score 421; DB 13; Length 1830;
Best Local Similarity 75.9%; Pred. No. 1.9e-103;
Matches 520; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 967 GGGATAAAAACTCTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGGCT 1026
DB 4 GGCATACGAACTGTGGCAGGATGGGATTAATGAAATTAATTCCTGATCAAGAGGCG 63
QY 1027 CACAAACGGGAATGAGGTGATCCTCGATGTTCTTTCAACCATACAGCTGAGGGTAAT 1086
DB 64 CACAAACGGAATAGAGGTATCATGATGTTGTTTCAATCATACAGCTGAGGGTAAT 123
QY 1087 GAGAAATGTCOAATTAATCAATTAAGGGGTGCAATTAATCACTATATGCTTGCA 1146
DB 124 GAGAATGTCCTCAATTTCTTTTCAGAGGTGTCACAAACAGTATGATTATCATGTTAGCA 183
QY 1147 CCCAAGGAGAGTTTATAACTATCTGCGTGTGGGAATACCTTCAACTGTAATCATCT 1206
DB 184 CCCAAGGGGAGTTCTATAACTATTCAGGATGTGGGAACAGTTCAATTCACACCATCA 243
QY 1207 GTGGTTCGTAATTCATTGTAGATGTTTAAAGATATCGGGTACGGAAATGCAATGTGAT 1266
DB 244 GTTGTGCGACAAATTAATGTTGACTTAAAGATATTGGGTAAACAGAAATGCACGTGGAT 303
QY 1267 GGTTCGTTTGTGATCTGCATCATATGACCAAGAGGTTCCAGTCTGTGGGATCCAGTT 1326
DB 304 GGTTCGTTTGTGATCTGCTTCTTATTATGACCAAGGATAGCAGTCTCTGGGATGAGCT 363
QY 1327 AACGTGTATGAGGTCCCAATAGAAAGGTGACATGATCAACACAGGACACCTCTTGTACT 1386
DB 364 AATGTAATTTGGTCTCCCAATAGAAAGTGACTTTGTTGACACAGGAACCCCTCTAAGCAGC 423
QY 1387 CCACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
DB 424 CCACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 1447 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 1506
DB 484 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 543
QY 1507 TCTGAGTGGAAATGGGAAGTACCGGGAATGTCGGTCAATTCATTAAGGCACTGATGGA 1566
DB 544 TCAGAAATGGAAATGGGAAGTATAGACACCGGTGGCTGTTTATCAAGGGTACAGATGGC 603
QY 1567 TTTGCTGTGGTTTGGCGAATGCTTTTGTGGAGTCCACACCTATACAGGTAAGTTGT 1626
DB 604 TTTGCTGTGGTTTGGCGAATGCTTTTGTGGAGTCCACACCTATACAGGTAAGTTGT 663
QY 1627 GGCAATCTTGAATGAGTTGAGT 1651
DB 664 AGAAACCGTGGCATAGTATTAACCT 688

RESULT 12

US-10-424-599-11817
; Sequence 11817, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 11817
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110679C.1
US-10-424-599-11817

Query Match 14.0%; Score 421; DB 13; Length 2052;
Best Local Similarity 75.9%; Pred. No. 2.1e-103;
Matches 520; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 967 GGGATAAAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGGCT 1026
DB 4 GGCATACGAACTGTGGCAGGATGGGATTAATGAAATTAATTCCTGATCAAGAGGCG 63
QY 1027 CACAAACGGGAATGAGGTGATCCTCGATGTTCTTTCAACCATACAGCTGAGGGTAAT 1086
DB 64 CACAAACGGAATAGAGGTATCATGATGTTGTTTCAATCATACAGCTGAGGGTAAT 123
QY 1087 GAGAAATGTCOAATTAATCAATTAAGGGGTGCAATTAATCACTATATGCTTGCA 1146
DB 124 GAGAATGTCCTCAATTTCTTTTCAGAGGTGTCACAAACAGTATGATTATCATGTTAGCA 183
QY 1147 CCCAAGGAGAGTTTATAACTATCTGCGTGTGGGAATACCTTCAACTGTAATCATCT 1206
DB 184 CCCAAGGGGAGTTCTATAACTATTCAGGATGTGGGAACAGTTCAATTCACACCATCA 243
QY 1207 GTGGTTCGTAATTCATTGTAGATGTTTAAAGATATCGGGTACGGAAATGCAATGTGAT 1266
DB 244 GTTGTGCGACAAATTAATGTTGACTTAAAGATATTGGGTAAACAGAAATGCACGTGGAT 303
QY 1267 GGTTCGTTTGTGATCTTGCATCATATGACCAAGAGGTTCCAGTCTGTGGGATCCAGTT 1326
DB 304 GGTTCGTTTGTGATCTGCTTCTTATTATGACCAAGGATAGCAGTCTCTGGGATGAGCT 363
QY 1327 AACGTGTATGAGGTCCCAATAGAAAGGTGACATGATCAACACAGGACACCTCTTGTACT 1386
DB 364 AATGTAATTTGGTCTCCCAATAGAAAGTGACTTTGTTGACACAGGAACCCCTCTAAGCAGC 423
QY 1387 CCACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
DB 424 CCACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 1447 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 1506
DB 484 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 543
QY 1507 TCTGAGTGGAAATGGGAAGTACCGGGAATGTCGGTCAATTCATTAAGGCACTGATGGA 1566
DB 544 TCAGAAATGGAAATGGGAAGTATAGACACCGGTGGCTGTTTATCAAGGGTACAGATGGC 603
QY 1567 TTTGCTGTGGTTTGGCGAATGCTTTTGTGGAGTCCACACCTATACAGGTAAGTTGT 1626
DB 604 TTTGCTGTGGTTTGGCGAATGCTTTTGTGGAGTCCACACCTATACAGGTAAGTTGT 663
QY 1627 GGCAATCTTGAATGAGTTGAGT 1651
DB 664 AGAAACCGTGGCATAGTATTAACCT 688

RESULT 13

US-10-425-114-15962

Db 991 ATGTGTGGACTGTCTGGGATCTGGACAGCGAATTTTCATATTGATGTTTTGCGTTT 1050
Qy 1279 GATCTTGCATCAATAATGACAGAGGTTCCAGTCTGGGATCCAGTTAAGTATGGA 1338
Db 1051 GATTAGCCTCTATTTTGGGAAGGATCCCTG----- 1082
Qy 1339 GCTCCAATAGAAGTGACATGATCAACACAGGACACCTCTTGTTACTCCACCACCTATT 1398
Db 1083 -----GGGCTACCCCTTGGCAATCCCTCTTTG 1113
Qy 1399 GACATGATCAGCAATGACCCAAATCTTGGAGGCGTCAAGCTCATTTGCTGAAGCATGGAT 1458
Db 1114 GAAACCCCTGGCTTTGATCCCATTTTGGCCCGTTCCAACTTATTGCTGAAGCCTGGAT 1173
Qy 1459 GCAGAGGCGCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGTGAAT 1518
Db 1174 GCGGTGGCTATACCAAGTAGGATCTTTCCAGTTATGGCCGCTGGCCGAATGGAAT 1233
Qy 1519 GGSAAATACCGGACATTTGCGTCAATTCATTAAGGCACTGATGGAATTTGCTGTGGT 1578
Db 1234 GGGAAATACCGAGATACGGTCCGAAATTTATTAAAGGAGATCGGGGTAAATTGGGAA 1293
Qy 1579 TTTGCCGATGCTTTTGGAGTCCACACTATACAGGTA 1620
Db 1294 ATGCCCAAGGCTACAGGGTTCCCGGACCTTTATCAAGGA 1335

RESULT 15

US-10-425-114-7405
; Sequence 7405, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7405
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700659189_FLI
US-10-425-114-7405

Query Match 6.3%; Score 187.8; DB 13; Length 815;
Best Local Similarity 65.8%; Pred. No. 5.1e-40;
Matches 273; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
Qy 2505 TCTGAGTGCACCGATTCTGTGCTCATGACCAAAATTCGCAAGGAGTGGAGGCTTT 2564
Db 3 TCAGACTTCTTCAGATTTTGGCTTATGACTAAGTTCGCGAGGAATGTGAATCGCTA 62
Qy 2565 GGCCTTGAGGACTTTTCCAAACGGCAACGGCTGAGTGGATGGTTCATCAGCTGGGAAG 2624
Db 63 GGCCTAGCTGACTTCCCAACCTCTGAGAGGCTGAGTGGCATGGTCAATTTCTCGAAAG 122
Qy 2625 CCTGATGGTCTGAGATAGCCGATTCGTCCTTTTCCATGAAGATGAAGACAGGCG 2684
Db 123 CCAGACTGGTCTGAACACAGCGGTTTGTGGCTTGTACCATGGTAGATTCAAGTGAAGGGA 182
Qy 2685 GAGATCTATGTGGCTTTCAACACAGGCACTTACCGCGCTTTGTTGAGTCTCCAGAGCGC 2744
Db 183 GAAATATACATTTGCTTCAATATGAGTCATTTACCTTTACAGTTACCTTGGCGGAGCGT 242
Qy 2745 GCAGGGCGCGGTGGGAACCGGTGGTGGACACAGGCAAGCCAGCACCATAGACTTCCTC 2804

Db 243 CCTGGATACAAATGGGAACCTCTTTGTAGACACCAGCAAGCCTACACCATATGATTTCTCTC 302
Qy 2805 ACCGACGACTTACCTGATCGGCTCTACCATACACAGTTCTCGCATTTCTCTACTCC 2864
Db 303 ACTCCTGACCTTCTCTGGGAAGAGATATTGCCATACACAGTATGCTCAGTTTCTGGACGCC 362
Qy 2865 AACCTCTACCCCATGCTCAGCTACTCATCGGTCTCCTAGTATTGCGCCCTGATG 2919
Db 363 AATATGATATCCATGCTTAGTTATTCTTCATTATCTCTTGGCAATCCAGATG 417

Search completed: August 10, 2004, 01:20:08
Job time : 1308 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2004, 14:46:38 ; Search time 7308 Seconds
(without alignments)
12246.436 Million cell updates/sec

Title: US-09-674-817B-2

Perfect score: 2997

Sequence: 1 ggtcggcgccggcgccgcg.....aaaaaaaaaaaaaaaaaaaaa 2997

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_lam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
c 1	623.2	20.8	910	13	BQ609719
2	581.8	19.7	737	13	BQ609582
3	580.4	19.7	625	14	CD897285
4	565.4	18.9	617	13	BU997255

5	556.6	18.6	590	12	BJ267405
6	525.4	17.5	578	10	BZ493792
7	498.2	16.6	536	13	BU971724
8	485.4	16.2	519	13	BU970613
9	479.4	16.0	508	14	CD890597
c 10	468.4	15.6	564	12	BJ272361
11	452.4	15.1	697	14	CA199345
12	431.2	14.4	622	14	CF041929
13	414.2	13.8	445	13	BU974414
14	408.4	13.6	438	13	BU971179
15	407.6	13.6	438	13	BU971450
c 16	407	13.6	591	14	CB605134
c 17	405.6	13.5	584	14	CB877804
c 18	403.8	13.5	474	14	CD890598
c 19	396	13.2	644	9	AI737641
c 20	393.2	13.1	551	14	CB617184
c 21	390.2	13.0	913	12	BZ444934
c 22	390	13.0	435	10	BZ425551
c 23	379.2	12.7	475	13	BQ167195
c 24	379.2	12.7	477	13	BQ609691
c 25	378.4	12.6	753	13	BQ865760
c 26	366.2	12.2	479	14	CB858538
27	350	11.7	431	12	BM500514
28	346	11.5	561	13	BU933907
29	342.2	11.4	423	13	BU974906
30	328	10.9	469	12	BI075394
31	324.4	10.8	496	14	CF040681
32	319.6	10.7	655	14	CB035933
c 33	319	10.6	574	9	AI901664
34	315	10.5	497	14	CD442761
c 35	314.6	10.5	582	13	BU043560
c 36	311	10.4	675	13	CA109043
37	305.6	10.2	592	12	BI934640
38	303.2	10.1	580	12	BI934559
c 39	291.4	9.7	785	12	BJ591026
c 40	285.2	9.5	473	14	CK101133
41	278.6	9.3	558	10	AW832588
42	271.8	9.1	547	12	EM178903
c 43	270.8	9.0	781	14	CD576563
c 44	270.6	9.0	729	12	BU595165
c 45	263.4	8.8	669	14	CD003812

ALIGNMENTS

RESULT 1
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LOCUS BQ609719 910 bp mRNA linear EST 25-JUN-2002
DEFINITION BRY 5805 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.
ACCESSION BQ609719
VERSION BQ609719.1 GI:21559058
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 910)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST sequences
JOURNAL Arabidopsis Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.

FEATURES		Location/Qualifiers	
source			
	1. .910		
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	/cultivar="Wyuna"		
	/db_xref="taxon:4565"		
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	/dev_stage="developing endosperm tissue 8, 10 and 12 DPA (days post anthesis)"		
	/clone_lib="wheat EST endosperm library"		
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	Best Local Similarity	96.1%;	Pred. No. 8.2e-66;
	Matches 692; Conservative	0;	Mismatches 23; Indels 5; Gaps 5;
QY	401	GGGTGACCGAGGAGGTTCCCTTGACCCCTCATGAATCGGACC-CGGAAACCTGTGGCAT	459
DB	720	GGGTTCCCAAGGAGGTCCCTTGACCCCTAATGAATCGGACC-CGGGAAAGGTGTGGCAT	661
QY	460	GTCTTT-CATCGAAGGCGAGCTGCACAACATGCTTTACGGGTACAGTTTCACGGCACCTTT	518
DB	660	GTTTTCCATGGAAGCAAGCTGCACAACATCTATTAA-CGGGAACAGGTTTCGACGGCGCTTT	601
QY	519	TGCTCTCTCACTCGGGCAGCTACCTTCATGTTTCCCAATGTC-GTGGTGGATCCCTTATGCTTA	577
DB	600	TGTTCTCTCACTCGGGCCATACTTGTATGTTTCCAAAGTCGTGTGGATCCCTTATGCTTA	541
QY	578	AGGCAGTATAAGCCGAGGGG-AGTATGTTGTTCCAGCGCTGGTAACAAATTGCTGGCCT	636
DB	540	AGGCAGTATAAGCCGAGGGGAAGTATGTGTTCCAGCGCTGGTAACAAATTGCTGGCCT	481
QY	637	C-AGATGGCTGCATCATCTCTCCATATACGACGTTTGATTTGGAGAGGGGACCTACC	695
DB	480	CAAGATGGCTGGCATGATCCCTCTCCATATACGACGTTTGATTTGGAGAGGGGACCTACC	421
QY	696	TCTAAGATATCCTCAAAGGACCTGGTAAATATATGAGATGCATCTCGTGGATTACGAA	755
DB	420	TCTAAGATATCCTCAAAGGACCTGGTAAATATATGAGATGCATCTCGTGGATTACGAA	361
QY	756	GCATGATTCAAGCAATGTAGAACATCCGGTACTTTTCATTGAGCTGTGTCGAGGTTGA	815
DB	360	GCATGATTCAAGCAATGTAGAACATCCGGTACTTTTCATTGAGGCTGTGTCGAGGTTGA	301
QY	816	CTATTTGAAGGAGCTTTGGAGTTAAATTTGATTTGAATTAATGCCCTGCCATGAGTTCAACGA	875
DB	300	CTATTTGAAGGAGCTTTGGAGTTAAATTTGATTTGAATTAATGCCCTGCCATGAGTTCAACGA	241
QY	876	GTTGGAGTACTCAACCTCTCTTTCCAAGATGAACCTTTTGGGGAATTTTACCAATAACTTT	935
DB	240	GTTGGAGTACTCAACCTCTCTTTCCAAGATGAACCTTTTGGGGAATTTTACCAATAACTTT	181
QY	936	CTTTTCCACCAATGCAAGATACACATCAGCGGGATAAAAAA-CTGTGGCGTGTATGCCCAT	995
DB	180	CTTTTCCACCAATGCAAGATACACATCAGCGGGATAAAAA-CTGTGGCGTGTATGCCCAT	121
QY	996	AAATGAGTTCAAACCTTTTGTAAAGAGAGGCTCAAAACCGGGGAATTTGAGGTGATCCTGGA	1055
DB	120	AAATGAGTTCAAACCTTTTGTAAAGAGAGGCTCAAAACCGGGGAATTTGAGGTGATCCTGGA	61
QY	1056	TGTTGTCCTTCAACCATACAGCTGAGGGAATGAGATGTTGCCAATATATCATTTAAGG	1115
DB	60	TGTTGTCCTTCAACCATACAGCTGAGGGAATGAGATGTTGCCAATATGTCATTTAAGG	1
RESULT 2			
BQ609582		737 bp	mRNA linear EST 25-JUN-2002
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			

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Db 541 AGTGAATGGGAAGTACCGGACATTTGTGCGCAATTTCTTAAGGCACTGGTGGGATTT 600
QY 1570 GCTGGTGGTTTTCGGAATG--TCTTTGTGGAAGTCCACACCTAT 1612
Db 601 GTTGGTGGTTTTCGGAAGTCTTTTGTGAAGTCCACACCTAT 645

RESULT 3
CD897205
LOCUS
DEFINITION G174.105C12P010823 G174 Triticum aestivum cDNA clone G174105C12,
mRNA sequence.
ACCESSION CD897205
VERSION CD897205.1 GI:32671533
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
JOURNAL Poideae; Triticeae; Triticum.
COMMENT 1 (bases 1 to 625)

REFERENCE
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
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/cultivar="recital"
/db_xref="taxon:4565"
/clone="G174105C12"
/tissue_type="grain (174 degrees per day after
pollination)"
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ORIGIN
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Best Local Similarity 99.5%; Pred. No. 8.4e-62;
Matches 613; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 2258 CAACAGAGATGGAGAAATCACAATCTTAGCTGGAATTTGGGAGAGAGAAATTCGC 2317
Db 12 CAACAGAGATGGAGAAATCACAATCTTAGCTGGAATTTGGGAGAGAGAAATTCGC 71
QY 2318 AAGATTCTCTCAAAAGATTGAGAGAGGAGATGCGCAATTTCTTTGTTGTTCTCAT 2377
Db 72 AAGATTCTCTCAAAAGATTGAGAGAGGAGATGCGCAATTTCTTTGTTGTTCTCAT 131
QY 2378 GGTTCCTCAGGAGTTCGAATGTTCTACATGGGTGATGAATATGCGGCACACAAAAGGGG 2437
Db 132 GGTTCCTCAGGAGTTCGAATGTTCTACATGGGTGATGAATATGCGGCACACAAAAGGGG 191
QY 2438 CAACAAATACATACACTGCCATGATTTCTATGCAATTTTTCGCTGGGATATAAAGA 2497
Db 192 CAACAAATACATACACTGCCATGATTTCTATGCAATTTTTCGCTGGGATATAAAGA 251
QY 2498 ACAATCTCTGAGTTGACCGCATTTCTGCTGCTCATGACCAAAATTCGCAAGAGTGCGA 2557
Db 252 ACAATCTCTGAGTTGACCGCATTTCTGCTGCTCATGACCAAAATTCGCAAGAGTGCGA 311
QY 2558 GGGTCTTGGCCTTGAGGACTTTCCACGGCCAAACGGCTGAGTGGCATGGTCATCAGCC 2617
Db 312 GGGTCTTGGCCTTGAGGACTTTCCACGGCCAAACGGCTGAGTGGCATGGTCATCAGCC 371
QY 2618 TGGGAAGCCTGATTTGGTCTGAGATAGCCGATTGTCGCTTTTCCATGAAGTGAAG 2677

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Db 372 TGGGAAGCCTGATTTGGTCTGGAATAGCCGATTCGTTCCATGAAGATGAAG 431
QY 2678 ACAGGGCGAGATCTATGTGGCCTTCAACACAGCCACTTACCGGCGGTGTGTAGCTCCC 2737
Db 432 ACAGGGCGAGATCTATGTGGCCTTCAACACAGCCACTTACCGGCGGTGTGTAGCTCCC 491
QY 2738 AGAGCGCGAGGGCGCGGTGGGAACCGGTGGTGACACAGCAAGCCAGCACCATAGA 2797
Db 492 AGAGCGCGAGGGCGCGGTGGGAACCGGTGGTGACACAGCAAGCCAGCACCATAGA 551
QY 2798 CTTCTCTACCGAGACTTACCTGATCGCGCTCTCACCATACACCATGTTCTCGCATTTCT 2857
Db 552 CTTCTCTACCGAGACTTACCTGATCGCGCTCTCACCATACACCATGTTCTCGCA-TTCT 609
QY 2858 CTACTCCAAACCTCTAC 2873
Db 610 CTATCCAAACCTCTAC 625

RESULT 4
BU997255
LOCUS
DEFINITION HI07G18r HI Hordeum vulgare subsp. vulgare cDNA clone HI07G18
5-PRIME, mRNA sequence.
ACCESSION BU997255
VERSION BU997255.1 GI:24274238
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Poideae; Triticeae; Hordeum.
JOURNAL 1 (bases 1 to 617)
COMMENT Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 617 Std Error: 0.00
Plate: 7 row: G column: 18
Seq primer: M13rev.
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/clone_lib="HI"
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artifact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sall, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

ORIGIN
Query Match 18.9%; Score 565.4; DB 13; Length 617;
Best Local Similarity 95.7%; Pred. No. 8.6e-59;
Matches 581; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 421 CTTGACCCCTGATGAATCGGACCGGAACCTGTGGCATGTCTTTCATCGAAGCGAGCTG 480
Db 11 CTTGACCCCTGATGAATCGGACCTGGGACGCTGTGGCATGTCTTCTCGTGTGGGAGCTG 70
QY 481 CACAACATGCTTTAGGGGTACAGGTTGACGGACCTTGTCTCTACTCTGCGGGCACTAC 540
Db 71 CACGCGATGCTTTATGGGTACAGGTTGACGGACCTTGTCTCTACTCTGCGGGCACTAC 130
QY 541 CTTGATGTTTCCAAATGCTGGTGCATCTTATCTTAAGCAGTGAATAAGCCGAGGGAG 600
Db 131 TTTGATGTTTCCAAATGCTGGTGCATCTTATCTTAAGCAGTGAATAAGCCGAGGGAG 190
QY 601 TATGGTGTTCAGCGCGTGTGTAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT 660
Db 191 TATGGTGTTCAGCGCGCATGTAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT 250
QY 661 CCATATAGCAGTTTGAATGGGAAGGCGACCTACTCTTAAGATATCTTCAAAAGGACCTG 720
Db 251 CCATATAGCAGTTTGAATGGGAAGGCGACCTACTCTTAAAGATATCTTCAAAAGGACCTT 310
QY 721 GTAATATAGATGCACTTTCGCTGGATTCAGGAAGCATGATTCAGCAATGTAGAACAT 780
Db 311 GTAATATAGATGCACTTTCGCTGGATTCAGGAAGCATGATTCAGCAATGTAGAACAT 370
QY 781 CCGGTACTTTTCATGGAGCTGTGTCGAAGCTTGACTATTTGAAGGAGCTTGGAGTTAAT 840
Db 371 CCGGTACTTTTCATGGAGCTGTGTCGAAGCTTGACTATTTGAAGGAGCTTGGAGTTAAT 430
QY 841 TGTATTGAATTAATGCTGCTGATGAGTTCAGGAGCTGGAGTACTCAACCTCTTCTTCC 900
Db 431 TGTATTGAATTAATGCTGCTGATGAGTTCAGGAGCTGGAGTACTCAACCTCTTCTTCC 490
QY 901 AAGATGAACCTTTGGGATATCTACCAATAAACTTTTTCACCAATGACAGATACACA 960
Db 491 AAGATGAACCTTTGGGATATCTACCAATAAACTTTTTCACCAATGACAGATACACG 550
QY 961 TCAGCGGGATAAAAACTGTGGCGGTGATGCCATAATGAGTTCAAACTTTTGTGAAGA 1020
Db 551 TCAGGTGGATAAAAAACTGTGGCGGTGATGGCATAAACGAGTTCAAACTTTTGTGAAGA 610
QY 1021 GAGGCTC 1027
Db 611 GAGTCTC 617

RESULT 5
BU267405
LOCUS
DEFINITION
BU267405 Y. Ogihara unpublished cDNA library, wh_oh linear EST 09-APR-2002
aestivum cDNA clone wholif13 5', mRNA sequence.
ACCESSION
BU267405
VERSION
BU267405.1 GI:20087755
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 590)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasi Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 590
/organism="Triticum aestivum"

FEATURES
source

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/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wholif13"
/tissue_type="pistil at heading date"
/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_oh"

ORIGIN

Query Match      18.6%; Score 556.6; DB 12; Length 590;
Best Local Similarity 96.4%; Pred. No. 1e-57;
Matches 568; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2255 GAACAACAGAGATGGAGAAATCAATCTTGTAGCTGGAATTTGTGGGAGGAGAGAAATT 2314
Db 2 GAACAACAGAGATGGAGAAATCAATCTTGTAGCTGGAATTTGTGGGAGGAGAGAAATT 61
QY 2315 CGCAGATTTGCTGTCAAAAGATTGAGGAAGCAGATCGCAATTTCTTTGTTGTCT 2374
Db 62 CGCAGATTTGCTGTCAAAAGATTGAGGAAGCAGATCGCAATTTCTTTGTTGTCT 121
QY 2375 CATGTTTCTCAAGAGATTCCAATTTCTACATGGGTGATGAATATGSCCACAACAAAGG 2434
Db 122 CATGTTTCTCAAGAGATTCCAATTTCTATATGGCGATGAGTATGGCCACACAAAGG 181
QY 2435 GGGCAACAACATACATACCTGCCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 2494
Db 182 GGGCAACAACATACATACCTGCCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 241
QY 2495 AGAACAATACTCTGAGTTGACCGGATTTCTGCTGCTCATGACCAAAATTCGCCAAGGAGTG 2554
Db 242 AGAACAATACTCTGAGTTGACCGGATTTCTGCTGCTCATGACCAAAATTCGCCAAGGAGTG 301
QY 2555 CGAGGCTCTTGGCTTGGAGACTTTCCAAAGCCAAACGGCTGAGTGGCATGTGTCATCA 2614
Db 302 CGAGGCTCTTGGCTTGGAGACTTTTCCAAAGCCAAACGGCTGAGTGGCATGTGTCATCA 361
QY 2615 GCTCGGAGGAGCTGATTTGCTGAGATAGCCGATTTGCTGCTTTTCCATGAAGATGA 2674
Db 362 GCTCGGAGGAGCTGATTTGCTGAGATAGCCGATTTGCTGCTTTTCCATGAAGATGA 421
QY 2675 AAGACAGGCGGAGATCTATGTCGCTTCAACACGAGCAGTTACCGCGCTTGTGAGCT 2734
Db 422 AAGACAGGCGGAGATCTATGTCGCTTCAACACGAGCAGTTACCGCGCTTGTGAGCT 481
QY 2735 CCCAGAGCGCGAGCGGCGCTGGGAACCGGTGGACACGAGCAGCAGCAGCAGCAGCAG 2794
Db 482 CCCAGAGCGCGAGCGGCGCTGGGAACCGGTGGACACGAGCAGCAGCAGCAGCAGCAGCAG 541
QY 2795 CGACTTCTCCACGAGCAGTTTACCTGATCGGCTCTCACCATACACAG 2843
Db 542 CGACTTCTCCACGAGCAGTTTACCTGATCGGCTCTCACCATACACAG 590

RESULT 6
BU493792
LOCUS
DEFINITION
BU493792 WHE1275_E05_I09ZS Secale cereale anther cDNA library Secale cereale
cDNA clone WHE1275_E05_I09, mRNA sequence.
ACCESSION
BU493792
VERSION
BU493792.1 GI:9660385
KEYWORDS
EST.
SOURCE
Secale cereale (rye)
ORGANISM
Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Secale.
1 (bases 1 to 578)
Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J.,
Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y.,
Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and
Tong, J.C.
The structure and function of the expressed portion of the wheat

TITLE

```

genomes - Anther cDNA library from rye
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818
 Email: andersn@wp.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.

FEATURES

Location/Qualifiers

1..578
 /organism="Secale cereale"
 /mol_type="mRNA"
 /cultivar="Blanco"
 /db_xref="taxon:4550"
 /clone="WHE1275.E05.I09"
 /tissue_type="Anther"
 /dev_stage="Adult plant before anthesis"
 /lab_host="E. coli SOLR"
 /clone_lib="Secale cereale anther cDNA library"
 /note="Vector: lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
 greenhouse. Anthers were harvested and pooled from early
 meiosis to late meiosis. The tissue, total RNA, and
 poly(A) RNA were prepared (Butler, Ross and Gustafson) at
 University of Missouri, Columbia. A cDNA library was
 made, and the cDNA clones were in vivo excised to give
 pBluescript phagemids in the TJ Close lab (Choi, Close,
 Fenton) at the University of California, Riverside.
 Plasmid DNA preparations and DNA sequencing were performed
 in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 17.5%; Score 525.4; DB 10; Length 578;
 Best Local Similarity 95.3%; Pred. No. 5.6e-54;
 Matches 552; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 2251 GGGAGAACACAGAGATGGAGAAATCACAAATCTTAGCTGGAATTTGGGGAGAGGAG 2310
 Db 1 GAGGGGACACAGAGATGGAGAAAT-ACAATCTTAGCTGGAATTTGGGGAGAGGAG 59
 QY 2311 AATTGCGAAGATTTCTGTCAAAAGATTGAGGAGAGGCGAGATTCGCGCAATTTCTTTGTTT 2370
 Db 60 AATTGCGAAGATTTCTAGTCAAAAGATTGAGGAGAGGCGAGATTCGCGCAATTTCTTTGTTT 119
 QY 2371 GTCTCATGTTTCTCAAGAGATTCCTCAATGTTTACATGGGTGATGAATATGGCCACAA 2430
 Db 120 GTCTCATGTTTCTCAAGAGATTCCTCAATGTTTACATGGGTGATGAATATGGCCACAA 179
 QY 2431 AAGGGGCAACAAATACATCTGCGCATGATCTTATGTCAATTTTTCGCTGGGATA 2490
 Db 180 AAGGGGCAACAAATACATCTGCGCATGATCTTATGTCAATTTTTCGCTGGGATA 239
 QY 2491 AAAAAGAACAAATCTCTGAGTTGCGACCGATTCGTCGCTCATGACCAAAATTCGCAAGG 2550
 Db 240 AAAAAGAACAAATCTCTGAGTTGCGACCGATTCGTCGCTCATGACCAAAATTCGCAAGG 299
 QY 2551 AGTCGAGGGTTTGGCTTGGAGACTTCCACGGCCAAACGCTGCAGTCGATGGTC 2610
 Db 300 AGTCGAGGGTTTGGCTTGGAGACTTCCACGGCTGACGCTGTCAGTCGATGGTC 359
 QY 2611 ATCAGCTGGGAAGCCCTGATTTGCTGAGAAATAGCCGATTCGTTGCCCTTTTCCATGAAAG 2670
 Db 360 ATCAGCTGGGAAGCCCTGATTTGCTGAGAAAGCCGATTCGTTGCCCTTTTCCATGAAAG 419
 QY 2671 ATGAAACACAGGCGAGATCTATGTGCGCTTCAACACAGCCACTTACCGGCGTTGTTG 2730
 Db 420 ATGAAACAAAGGTGAGATCTATGTGCGCTTCAACACAGCCACTTACCGGCGTTGTTG 479
 QY 2731 AGCTCCACAGCGCGGCGCGCGGTGGGAAACCGGTGGTGGACACAGGCAAGCCAGCAC 2790

Db 480 AACTCCAGAGCGCAGCGCACCGGTGGACACCGGTGGACACAGAAAGGAGCAC 539
 QY 2791 CATAGCACTTCTCACCAGCAGCTTACCTGATCGGCTC 2829
 Db 540 CATATGACTTCTCACCAGCAGCTTACCTGATCGGCTC 578

RESULT 7
 BU9711724
 LOCUS
 DEFINITION
 BU9711724
 5-PRIME mRNA sequence.
 ACCESSION
 BU9711724
 VERSION
 BU9711724.1
 GI:24222517
 SOURCE
 EST.
 ORGANISM
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poaceae; Triticeae; Hordeum.
 1 (bases 1 to 536)
 Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.
 Barley ESTs from developing seeds
 Unpublished (2002)
 CONTACT: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 536 Std Error: 0.00
 Plate: 19 row: H column: 15
 Seq primer: M13rev.

FEATURES
 Location/Qualifiers
 1..536
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="GABI:238560"
 /db_xref="taxon:112509"
 /clone="HB19H15"
 /tissue_type="developing caryopsis"
 /dev_stage="8-15 DAP (days after pollination)"
 /lab_host="XL10-Gold"
 /clone_lib="BC"
 /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
 cDNA); Site_2: XhoI (3'-end of cDNA); developing
 caryopsis, 8-15 DAP(days after pollination) Due to a
 cloning artefact caused by the kit, in most cases the
 EcoRI site is NOT present, as well as the EcoRI adapter
 used for cloning. To excise the insert, restriction sites
 upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
 NOTE: Also due to the cloning system used Blue/white
 selection for recombinants is not 100% reliable."

ORIGIN
 Query Match 16.6%; Score 498.2; DB 13; Length 536;
 Best Local Similarity 96.6%; Pred. No. 1.1e-50;
 Matches 509; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 503 GTTTCGACGGCACCTTCTCTCACTCGGGCACTACCTGATTTTCCAATGTCGGG 562
 Db 10 GTTTCGACGGCACCTTCTCTCACTCGGGCACTACCTGATTTTCCAATGTCGGG 69
 QY 563 TGTATCTTATGCTAAGCAGTGATAAGCCGGAGGATGCTGTTCCAGCGGTGTA 622
 Db 70 TGTATCTTATGCTAAGCAGTGATAAGCCGGAGGATGCTGTTCCAGCGGTGTA 129
 QY 623 ACAATTGCTGGCCTCAGATGGCTGATGCCCTCTTCCATATAGCAGTTTGAATGGG 682

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G11815A13"
/tissue_type="grain (118 degrees per day after
pollination)"
/clone_lib="G118"

ORIGIN

Query Match 16.0%; Score 479.4; DB 14; Length 508;
Best Local Similarity 97.8%; Pred. No. 2e-48;
Matches 486; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 443 CCGGACGCTGTGCGCATGCTTTCATCGAAGCGAGCTGCACACATGCTTTACGGGTACA 502
DB 12 CTGGGAACGATGCGCATGCTTTCATCGAAGCGAGCTGCAGGACATGCTTTACGGGTACA 71
QY 503 GGTTCGAGCGGCACCTTTGCTCCTCACCTGCGGCGACTACCTTGATGTTTCCAAATGTCGTGG 562
DB 72 GGTTCGAGCGGCACCTTTGCTCCTCACCTGCGGCGACTACCTTGATGTTTCCAAATGTCGTGG 131
QY 563 TGGATCCTTATGCTAAGCGAGTGTATAGCCGAGGGAGTATGTTTCCAGCGCGTGGTA 622
DB 132 TGGATCCTTATGCTAAGCGAGTGTATAGCCGAGGGAGTATGTTTCCAGCGCGTGGTA 191
QY 623 ACAATTCGTGCGCTCAGATGCGGTGATGATCCCTCTTCCATATAGCACGTTTGGTGG 682
DB 192 ACAATTCGTGCGCTCAGATGCGGTGATGATCCCTCTTCCATATAGCACGTTTGGTGG 251
QY 683 AAGCGACCTACCTCTTAAGATATCCTCAAAAGGACCTGGTAAATATATGAGATGCATTCG 742
DB 252 AAGCGACCTACCTCTTAAGATATCCTCAAAAGGACCTGGTAAATATATGAGATGCATTCG 311
QY 743 GTGGATTCACGACGATGATCAAGCAATGCTCAAGCAATGAGCAATGAGCAATGAGCAATG 802
DB 312 GTGGATTCACGACGATGATCAAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAG 371
QY 803 TGTGCAAGCTTGACTATTTCGAAGGAGCTTGGAGTAAATGATTAATTAATGATTAATGATTA 862
DB 372 TGTGCAAGCTTGACTATTTCGAAGGAGCTTGGAGTAAATGATTAATTAATGATTAATGAT 431
QY 863 ATGAGTTCAAGGAGCTGGAGTACTCAACCTCTTCTTCCAAAGATGAATTTTGGGATATT 922
DB 432 ATGAGTTCAAGGAGCTGGAGTACTCAACCTCTTCTTCCAAAGATGAATTTTGGGATATC 491
QY 923 CTACCATAACTCTCTTT 939
DB 492 CTACCATAACTCTCTTT 508

RESULT 10

BJ272361/c 564 bp mRNA linear EST 09-APR-2002
LOCUS
DEFINITION
aestivum cDNA clone wholif13 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Expressed genes in Triticum aestivum
Ogihara, Y. and Murai, K.
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

FEATURES
source
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..564

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wholif13"
/tissue_type="pistil at heading date"
/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_oh"

ORIGIN

Query Match 15.6%; Score 468.4; DB 12; Length 564;
Best Local Similarity 95.5%; Pred. No. 4e-47;
Matches 512; Conservative 0; Mismatches 20; Indels 4; Gaps 3;
QY 2429 AAAAGGGGGCAACAATACATACATG-CCATGATTCCTATGTCAATATTTTCCTCGGG 2487
DB 564 AAAAGGGGGCAACAATACATACATACATCTGCCCATGATTCCTATGTCAATATTTTNGTGG 505
QY 2486 ATAAAAAGAAACAATCTCTGAGTTGACCGATTCCTGCTCATGACCAAAATTCGCA 2547
DB 504 ATAAAAAGAAACAATCTCTGAGTTGACCGATTCCTGCTCATGACCAAAATTCGCA 445
QY 2548 AGGAGTGGGAGGCTCTGCGCTTGAGGACTTTCACACGCGCAAAAC-GGCTGAGTGGCAT 2606
DB 444 AGGAGTGGGAGGCTCTGCGCTTGAGGACTTTCACACGCGCGGCTGAGTGGCAT 385
QY 2607 GGTCTATCAGCTTGGGAAGCCTGATTTGCTGAGAAATAGCCGATTCGTTGCCCTTTCCATG 2666
DB 384 GGTCTATCAGCTTGGGAAGCCTGATTTGCTGAGAAATAGCCGATTCGTTGCCCTTTCCATG 325
QY 2667 AAAGATGAAGACAGGCGGAGATCTATGTGGCTTCACACAGCCACTTACCGGCCCTT 2726
DB 324 AAAGATGAAGACAGGCGGAGATCTATGTGGCTTCACACAGCCACTTACCGGCCCTT 265
QY 2727 GTTGAGCTCCCAAGAGCGGCGCGGCGGAGTGGGAAACCGGTGGACACAGGCAAGCCA 2786
DB 264 GTTGAGCTCCCGAGCGGACAGGCGCGGTTGGGAAACCGGTGGACACAGGCAAGCCA 205
QY 2787 GCACATAGCATTCCTCACCAGACACTTACTGATTCGGCTCTCACCATACACAGTTC 2846
DB 204 GCACATAGCATTCCTCACCAGACACTTACTGATTCGGCTCTCACCATACACAGTTC 145
QY 2847 TCGCATTTCTCTACTTCCAACTTACCCCTGCTCAGCTACTCGTCTATCTCTAGTA 2906
DB 144 TCTCATTTCTCTCACTTCCAACTTACCCCTGCTCAGCTACTCGTCTATCTCTAGTA 85
QY 2907 TTGCGCCCTGATTTTGAGAGACCAATATATACAGTAAATAATATGCTATATGTA 2962
DB 84 TTGCGCCCTGATTTTGAGAGGC--GGATATACAGTAAATAATATGTAATATGTA 31
RESULT 11
CAL199345
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 697)
Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.
The libraries that made SUCET
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P


```

/clone lib="BC"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); developing
carypsopsis, 8-15 DAP (days after pollination) Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable."

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ORIGIN

```

Query Match      13.6%; Score 408.4; DB 13; Length 438;
Best Local Similarity 96.1%; Pred. No. 7.3e-40;
Matches 416; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 941 CACCAATGACAAGATACACATCAGGGGGGATAAAAACTGTGGCGTGATGCCATAAATG 1000
Db 4 CACGAGGACGAGATACACGTGAGTGGGATAAAAACTGTGGCGTGATGCCATAAAGC 63

Qy 1001 AGTTCAAACTTTTGAAGAGAGCTCAACAAAGGGGAATTGAGTGATCCTGGATGTTG 1060
Db 64 AGTTCAAACTTTTGAAGAGAGCTCAACAAAGGGGAATTGAGTGATCCTGGATGTTG 123

Qy 1061 TCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCAAATATTATCATTTAAGGGGGTGC 1120
Db 124 TCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCGATTTATCATTTAGGGGGTGG 183

Qy 1121 ATAATACATACATATATGCTTGCACCCAGGAGAGTTTATATACTATTCTGGCTGTG 1180
Db 184 ATAATACATACATATATGCTTGCACCCAGGAGAGTTTATATACTATTCTGGCTGTG 243

Qy 1181 GGAATACCTTCAAGTGAATCATCTGCTGCTGCTCAATTCATTTAGATTTGTTAAGAT 1240
Db 244 GGAATACCTTCAAGTGAATCATCTGCTGCTGCTCAATTTAGATTTGTTAAGAT 303

Qy 1241 ACTGGGTGACGGAATGATGTTGATGTTTTCGTTTGTGATCTTGATCCATAATGACCA 1300
Db 304 ACTGGGTGATGGAATGATGTTGATGTTTTCGTTTGTGATCTTGATCCATAATGACCA 363

Qy 1301 GAGTTTCCAGTCTGTGGATCCAGTTAAGTGTATGAGCTCCAAATAGAGTGACATGA 1360
Db 364 GAGTTTCCAGTCTGTGGATCCAAATTAAGTGTATGAGCTCCAAATAGAGTGACATGA 423

Qy 1361 TCACACAGGGACAC 1375
Db 424 TCACACAGGGACAC 438

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RESULT 15
BU971450
LOCUS BU971450 438 bp mRNA linear EST 22-OCT-2002
DEFINITION BU971450 BC Hordeum vulgare subsp. vulgare cDNA clone HB17K14
5-PRIME, mRNA sequence.
ACCESSION BU971450
VERSION BU971450.1 GI:24222243
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Hordeum.
1 (bases 1 to 438)
Rachuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de

```

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Insert Length: 438 Std Error: 0.00
Plate: 17 row: K column: 14
Seq primer: M13rev.
Location/Qualifiers
source
1. 438

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FEATURES

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source
1. 438
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/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:236284"
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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); developing
carypsopsis, 8-15 DAP (days after pollination) Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable."

```

ORIGIN

```

Query Match      13.6%; Score 407.6; DB 13; Length 438;
Best Local Similarity 96.7%; Pred. No. 9.1e-40;
Matches 416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 802 GTGTGGAAGCTTGACTATTTGAAGAGCTTGGAGTTAATTGATTAATTAATGCCCTGC 861
Db 9 GGTTCGAAGCTTGACTATTTGAAGAGCTTGGAGTTAATTGATTAATTAATGCCCTGC 68

Qy 862 CATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCTTCAAGATGACTTTTGGGATAT 921
Db 69 CATGAGTTCAACGAGCTGGAGTATGCAACCTCTTCTTCAAGATGACTTTTGGGATAT 128

Qy 922 TCTACCAATAAACTTCTTTTCCCAATGACAAGATACACATCAGCGGGGATAAAAACTGT 981
Db 129 TCTACCAATAAACTTCTTTTCCCAATGACAAGATACACATCAGCGGGGATAAAAACTGT 188

Qy 982 GGGCGTGAATGCCATAAATAGATTCAAAACCTTTTGTAAAGAGAGGCTCAAAACCGGGAAAT 1041
Db 189 GGGCGTGAATGCCATAAAGAGTTCAAAACCTTTTGTAAAGAGAGTTCAAAACCGGGAAAT 248

Qy 1042 GAGTGATCCTGGATGTTGTTCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCAATA 1101
Db 249 GAGTGATCCTGGATGTTGTTCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCAATA 308

Qy 1102 TTATCATTTAAGGGGGTGCATAATACATACATATATGTTTGCACCCAGGAGAGTTT 1161
Db 309 TTATCATTTAAGGGGGTGCATAATACATACATATATGTTTGCACCCAGGAGAGTTT 368

Qy 1162 TATAACTATTCTGCTGTGGGAATACCTTCAACTGTAAATCATCTGTGGTTGTCATTC 1221
Db 369 TATAACTATTCTGCTGTGGGAATACCTTCAACTGTAAATCATCTGTGGTTGTCATTC 428

Qy 1222 ATTGTAGATT 1231
Db 429 ATTGTAGATT 438

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Search completed: August 9, 2004, 22:04:07
Job time : 7312 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: August 9, 2004, 22:08:10 ; Search time 7673 Seconds
(without alignments)
4315.662 Million cell updates/sec

Title: US-09-674-817B-3
Perfect score: 4212
Sequence: 1 SGPAPLRWRPNATAGKV.....SNLYPMLSYSVILVLRPDV 764

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674817@cgn 1 1 4892 @runat_04082004.165844.24581 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: 1: gb_ba: 2: gb_btg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vi: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un:

29: em_vi: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htg_mus: 34: em_htg_pln: 35: em_htg_rnd: 36: em_htg_mam: 37: em_htg_vrt: 38: em_by: 39: em_htgo_hum: 40: em_htgo_mus: 41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4203	99.8	2590	8	AF438328	AF438328 Triticum
2	4154	98.6	2490	8	TAE301647	TAE301647 Triticum
3	4148	98.5	2437	6	AX010486	AX010486 Sequence
4	4120.5	97.8	2574	8	AF548380	AF548380 Triticum
5	4050	96.2	2997	6	AX010481	AX010481 Sequence
6	4050	96.2	2997	6	AX010482	AX010482 Sequence
7	4050	96.2	2997	8	TAE307689	TAE307689 Triticum
8	4015.5	95.3	2495	8	AF490375	AF490375 Hordeum v
9	4005.5	95.1	2584	8	AB074189	AB074189 Hordeum v
10	3988.5	94.7	2445	8	AF490376	AF490376 Hordeum v
11	3586	85.1	2288	8	AB015615	AB015615 Oryza sat
12	3569.5	84.7	2700	6	A3427894	A3427894 Sequence
13	3528.5	83.8	2712	6	AR072143	AR072143 Sequence
14	3528.5	83.8	2712	6	ZMU18908	U18908 Zea mays Su
15	3029	71.9	2706	6	AR241384	AR241384 Sequence
16	3029	71.9	2706	6	AX006091	AX006091 Sequence
17	3029	71.9	2706	6	BD080223	BD080223 Starch de
18	3029	71.9	2706	8	AV132996	AV132996 Solanum t
19	3001	71.2	1708	8	AF143589	AF143589 Hordeum v
20	2923	69.4	2806	6	AR241388	AR241388 Sequence
21	2923	69.4	2806	6	BD080227	BD080227 Starch de
22	2923	69.4	2806	6	AX031277	AX031277 Sequence
23	2918	69.3	1706	6	AX505523	AX505523 Sequence
24	2895.5	68.7	2352	6	AX651353	AX651353 Sequence
25	2895.5	68.7	2352	8	BT010348	BT010348 Arabidops
26	2895.5	68.7	2352	8	BT000443	BT000443 Arabidops
27	2895.5	68.7	2694	8	AF548379	AF548379 Aegilops
28	2800	66.5	9643	8	AF548379	AF548379 Aegilops
29	2612	62.0	2133	6	A93395	A93395 Sequence 1
30	2612	62.0	2133	6	AR161657	AR161657 Sequence
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32	2493.5	59.2	10209	8	AB093426	AB093426 Oryza sat
33	2359.5	56.0	9289	6	AX031278	AX031278 Sequence
34	2359	53.6	1501	8	AF490377	AF490377 Hordeum v
35	2256	53.6	1517	8	AF438329	AF438329 Triticum
36	2234	53.0	11779	8	AF030882	AF030882 Zea mays
37	2328	52.9	10753	8	AV146807	AV146807 Zea mays
38	2328	52.9	10817	8	AV146808	AV146808 Zea mays
39	2318	52.7	10733	8	AV146812	AV146812 Zea mays
40	2318	52.7	10835	8	AV146811	AV146811 Zea mays
41	2206	52.4	10851	8	AV146810	AV146810 Zea mays
42	2165.5	51.4	10855	8	AV146800	AV146800 Zea mays
43	2152.5	51.1	10839	8	AV146796	AV146796 Zea mays
44	2152.5	51.1	10856	8	AV146791	AV146791 Zea mays
45	2152.5	51.1	10856	8	AV146797	AV146797 Zea mays

ALIGNMENTS

RESULT 1

AF438328 2590 bp mRNA linear PLN 13-NOV-2001
 LOCUS
 DEFINITION Triticum aestivum isoamylase precursor, mRNA, complete cds,
 alternatively spliced.
 ACCSSION AF438328
 VERSION AF438328.1 GI:16905062
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 2590)
 AUTHORS Netphan,S., Khandelwal,R.L. and Chibbar,R.N.
 TITLE Characterization of isoamylase transcripts produced during wheat
 grain development and germination
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2590)
 AUTHORS Netphan,S., Khandelwal,R.L. and Chibbar,R.N.
 TITLE Direct Submission
 JOURNAL Submitted (22-Oct-2001) Plant Biotechnology Institute, 110
 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada
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 Best Local Similarity: 99.74% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 8 Gaps: 0
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 Qy 21 GlyGluValCysAlaAlaValGluAlaAlaThrLysValGluAspGluGlyGluGlu 40

Db 152 GCGAGGTGTGCGCGCGGTGTTCAGAGCGCGCAGAGGTAGAGGACGAGGGGAGGAG 211
 Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGly 60
 Db 212 GACGAGCGCGTGGCGGAGGAGGTACCGCTCGCGCGCGGTGCAGGGTGTCTCCCGGA 271
 Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80
 Db 272 ATGCCCGCGCTGGCGCGCACCGCTCGCGCGCGGTCAATTCGCGCTATTTC 331
 Qy 81 GlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArg 100
 Db 332 GCGGAGCCACCGCGCGCGCTCTGCTCTTCACGCGAAGATCTCAAGCGGATAGG 391
 Qy 101 ValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisVal 120
 Db 392 GTGACCGAGGAGGTTCCTTGACCCCTGATGATCGGACCGGAGACGTGTCATGTC 451
 Qy 121 PheLeuGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAla 140
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QY 701 GluLeuProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysProAla 720
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QY 761 ArgProAspVal 764
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TAE301647 2490 bp mRNA linear PLN 04-JUN-2003
LOCUS Triticum aestivum mRNA for isoamylase (isol gene).
DEFINITION AJ301647
ACCESSION AJ301647.1 GI:17932897
VERSION isol gene; isoamylase.
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
1
REFERENCE
AUTHORS Genschel, U., Gernot, A., Lorz, H. and Lueticke, S.
TITLE The sugary-type isoamylase in wheat: tissue distribution and subcellular localisation
JOURNAL Online Publication
REMARK Planta, DOI 10.1007/s00425-001-0691-3
REFERENCE 2 (bases 1 to 2490)
AUTHORS Genschel, U.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-2000) Genschel U., Institut fuer Allgemeine Botanik, AMP II, Universitaet Hamburg, Ohnhorststrasse 18, Hamburg, 22609, Germany
REMARK revised by submitter 22-MAR-2001
COMMENT Related entry AJ307689.
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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	2490
Score:	4154.00	Matches:	751

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 Db 2232 TAGACCTTCCTACTGACGACTTACCTGATCGCGCTCTCACCATACACCGAGTCTCTCAT 2291
 QY 742 PheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArg 761
 Db 2292 TTCCTCAACTCCAACTCTACCCCATGCTCAGCTACTCATCGTCTCATCTAGTATTGGCG 2351
 QY 762 ProAspVal 764
 Db 2352 CCTGATGTT 2360

RESULT 3
 AX010486
 LOCUS AX010486 2437 bp DNA linear PAT 06-SRP-2000
 DEFINITION Sequence 6 from Patent WO9958690.
 ACCESSION AX010486
 VERSION AX010486.1 GI:9997329
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Luettkie, S., Abel, G., Loerz, H. and Genschel, U.
 TITLE Nucleic acid molecules which code for enzymes derived from wheat
 and which are involved in the synthesis of starch
 JOURNAL Patent: WO 9958690-A 6 18-NOV-1999;
 LUTETICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);
 GENSCHEL ULRICH (DE); HORSCHT SCHERING AGREVO GMBH (DE)

FEATURES
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ORIGIN
 Alignment Scores:
 Pred. No.: 0 Length: 2437
 Score: 4148.00 Matches: 750
 Percent Similarity: 99.08% Conservative: 5
 Best Local Similarity: 98.43% Mismatches: 7
 Query Match: 98.48% Indels: 0
 DB: 6 Gaps: 0

US-09-674-817B-3 (1-764) x AX010486 (1-2437)

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 VERSION AF548380.1 GI:31096627
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 ORGANISM Triticum aestivum
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 2574)
 AUTHORS Rahman,S., Nakamura,Y., Li,Z., Clarke,B., Fujita,N., Mukai,Y.,
 Yamamoto,M., Regina,A., Tan,Z., Kawasaki,S. and Morell,M.
 TITLE The sugary-type isoamylase gene from rice and Aegilops tauschii:
 characterization and comparison with maize and Arabidopsis
 GENOME 46 (3), 496-506 (2003)
 REFERENCE 2 (bases 1 to 2574)
 AUTHORS Rahman,S., Li,Z., Clarke,B., Regina,A. and Morell,M.
 TITLE Direct Submission
 JOURNAL Submitted (26-SEP-2002) Plant Industry, CSIRO, Clunies Ross,
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US-09-674-817B-3 (1-764) x AF548380 (1-2574)

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ACCESSION AX010481
VERSION AX010481.1 GI:9997324
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE 1
AUTHORS Luetticke, S., Abel, G., Loerz, H. and Genschel, U.
TITLE Nucleic acid molecules which code for enzymes derived from wheat
and which are involved in the synthesis of starch
JOURNAL Patent: WO 9958690-A 1 18-NOV-1999;
LUETTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);
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Qy 287 rGlyGlyLysLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGl 307
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551 nLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValIysArgLeuAr 571
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RESULT 6

AX010482

LOCUS

AX010482

DEFINITION

Sequence 2 from Patent WO9958690.

ACCESSION

AX010482

VERSION

AX010482.1

KEYWORDS

GI:9997326

SOURCE

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

REFERENCE

1.

AUTHORS

Lueticke,S., Abel,G., Loerz,H. and Genschel,U.

TITLE

Nucleic acid molecules which code for enzymes derived from wheat

JOURNAL

and which are involved in the synthesis of starch

Patent: WO 9958690-A 2 18-NOV-1999;

LUETTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);

GENSCHEL JURICH (DE); HOECHST SCHERING AGREVO GMBH (DE)

FEATURES

Location/Qualifiers

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/cultivar="Florida"

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ORIGIN

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Pred. No.:

0

Length:

2997

[illegible]

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Qy	21	GlyGluValCysAlaIaValValGluAlaIaThrLysValGluAspGluGlyGluGlu	40
Db	63	GGCGAGGTGTTCGGCGCGGGTGTTCGAGCGCGCGACGAAGGTAGAGGACGAGGGGAGGAG	122
Qy	41	AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGly	60
Db	123	GACGAGCGGGTGGCGGAGGACAGGTACGCGTTCGGCGCGCGGTGAGGGTCTCGCCGGA	182
Qy	61	MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer	80
Db	183	ATGCCCGCGCGTGGCGCGCACCGCGTTCGCGCGCGGGTCAATTTTCGCGGTCTATTTC	242
Qy	81	GlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLys-----	97
Db	243	GGCGAGGCCACCGCGCGGCGCTCTGCGTCTTTCACGCCAGAAGATCTCAAGCGCGTGGG	302
Qy	97	-----	97
Db	303	TTGGCTCCCGAGTAGATTTCATCAGCTTTGGGTGGCGCGCGCCCTTTTTCGGGCGTG	362
Qy	98	-----Ala-AspArgValThrGluGluValProLe	107
Db	363	CAATTTAAGTTTTCCTACGCGCCAAATGCTCAGGATAGGTGACCGAGGAGGTTCGCT	422
Qy	107	uAspProLeuMetAsnArgThrGlyValAsnValTyrPheIleGluGlyGluLeuHi	127
Db	423	TGACCCCTGATGAATCGACCGGGAAGTGTGGCATGTCTTCATCGAAGCGAGCTGCA	482
Qy	127	SAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe	147
Db	483	CAACATGCTTTACGGGTACAGTTTCGACGGCACCTTTGCTCTCTCACTCGCGGCACACTACCT	542
Qy	147	uAspValSerAsnValValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyr	167
Db	543	TGATGTTTCCAAATGCTGTGTGGATCTCTATGCTAAGCAGTGTAAAGCCGAGGGAGTA	602
Qy	167	rGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPr	187
Db	603	TGGTGTTCACGGCGTGGTAACATTTGCTGGCCTCAGTGGCTGGCATGATCCCTCTTTC	662
Qy	187	oTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuVa	207
Db	663	ATATAGCACGTTTCATTTGGGAAGCGCACCTACCTCTAAGATATCTCAAAGAGCACTGGT	722
Qy	207	lIleTyrGluMethIstLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr	227
Db	723	AAATATATGAGATGCACCTTGGTGATTTACGAACATGATTTCAAGCAATGTAGAACATCC	782
Qy	227	oGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnC	247
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Db	903	GATGAACCTTTTGGGATATCTACCAATAAATCTCTTTTCACCAATGACAAGATACATC	962
Qy	287	rGlyGlyLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGl	307
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Qy	387	lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspPr	407
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Qy	407	oValAsnValTyrsGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuVa	427
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Qy 511 cTTPHisSerIleAsnPhValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTh 531

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RESULT 8

AF490375

LOCUS Hordeum vulgare isoamylase mRNA, complete cds. PLN 25-JUL-2002

DEFINITION

ACCESSION AF490375

VERSION AF490375.1 GI:21314274

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.

1 (bases 1 to 2495)

Burton, R.A., Jenner, H., Carrangis, L., Fahy, B., Fincher, G.B., Hylton, C., Laurie, D.A., Parker, M., Waite, D., van Wegen, S., Verhoeven, T. and Denyer, K.

Starch granule initiation and growth are altered in barley mutants that lack isoamylase activity

Plant J. 31 (1), 97-112 (2002)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE 22096154

PUBMED 12100486

REFERENCE 2 (bases 1 to 2495)

AUTHORS Burton, R.A., Denyer, K. and Fincher, G.B.

TITLE Direct Submission

JOURNAL Submitted (06-MAR-2002) Plant Science, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia

FEATURES

Location/Qualifiers

1..2495

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ORIGIN

Alignment Scores:

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Score: 4015.50 Matches: 724

Percent Similarity: 97.25% Conservative: 19

Best Local Similarity: 94.76% Mismatches: 20

Query Match: 95.33% Indels: 1

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Qy 22 GluValCysAlaAlaValValGluAlaAlaThrLysVal---GluAspGluGlyGluGlu 40

Db 202 GAGGTCTGCGCGCGCGCTCGAGCGCGCAGCAGGCGCGAGGAGGAGGAGGAGGAG 261

Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyAlaCysArgValLeuAlaGly 60

Db 262 GAGGAGCGCGTGGCTGAGGACAGGTATGCGCTCGAGCGCGCTGAGGAGTCTCGCCGGA 321

Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80

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Qy 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArg 100

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Qy 101 ValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyrHisVal 120

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221	Qy	SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeu	240
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1162	Db	AATACTACATCATATGCTTGCAACCACGAGAGATTTTATACTATTCTGGCTGTGGG	1221
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1282	Db	TGGGTGATGAAATGCATATTGATGGTTTTCGTTTTTGATCTTGTCATCCATAATGACCAGA	1341
401	Qy	GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle	420
1342	Db	GGTTCAGTCTGTGGGATCCAAATTAACGTGTATGGAGCTCCAAATAGAGGTGACATGATC	1401
421	Qy	ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle	440
1402	Db	ACAACGGGACACCTCTTGTTTACTCCACCACCTATTTCACATGATCAGCAATGACCCAATT	1461
441	Qy	LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGly	460
1462	Db	CTTGGAGCGCTCAAGCTCATTTGCTGAAGCATGGGATCGAGAGGCGCTCTATCAAGTAGGT	1521
461	Qy	GlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArg	480
1522	Db	CAGTTCCCTCACTGGAAATGTTGGTCTGAGTGGNATGGGAATGCCGGACATTTGCCGT	1581
481	Qy	GlnPheIleLysGlyThrAspGlyPheAlaGlyPheAlaGluCysLeuCysGlySer	500
1582	Db	CAATTCATTAAGGCATCTGATGATTTGCTGGTGTGTTCCGAATGCTCTTTTGTGAAGT	1641

Qy	501	ProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerLeuAsn	PheValCysAla	520
Db	1642	CCACAACTATACCAGGCAGCAGGAAGAAACCTTGGCACAGTATCAATTTGTATGTGCA	1701	
Qy	521	HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn	540	
Db	1702	CATGATGGATTACCTGGCTGATTGGTAACATATATACAAAGTACAAATTTACCAAT	1761	
Qy	541	GlyGluAsnAsnArgAspGlyGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly	560	
Db	1762	GGGGAGGACAAACAGAGATCGAGAAAAATCAAACTTTAGCTGGAACTGTGGGGAGGAAGGA	1821	
Qy	561	GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheVal	580	
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Qy	581	CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr	600	
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Qy	621	LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLys	640	
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Qy	721	ProTyrAspPheLeuThrAspAspLeuProAsArgAlaLeuThrIleHisGlnPheSer	740	
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Qy	761	ArgProAspVal	764	
Db	2422	CGCCCTGATGTT	2433	

RESULT	9
AB074189	
LOCUS	2584 bp mRNA linear PLN 14-NOV-2001
DEFINITION	Hordeum vulgare hviisol gene for isoamylase, complete cds.
ACCESSION	AB074189
VERSION	AB074189.1 GI:16923278
KEYWORDS	.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE	1
AUTHORS	Komatsu,A., Kato,T. and Komae,K.
TITLE	Isolation of isoamylase gene in barley
JOURNAL	Published Only in Database (2001)

Db 1498 CTTGGAGCGCTCAAGCTCATGCTGAAGCAGGATGCGAGGCGCTCTCTCAAGTAGCT 1557
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RESULT 10

LOCUS AF490376 2445 bp RNA linear PLN 25-JUL-2002
 DEFINITION Hordeum vulgare mutant isomylase precursor RNA, complete cds.
 ACCESSION AF490376
 VERSION AF490376.1 GI:21314276
 KEYWORDS

SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 2445)
 AUTHORS Burton,R.A., Jenner,H., Carrangis,L., Fahy,B., Fincher,G.B.,
 Hylton,C., Laurie,D.A., Parker,M., Waite,D., van Wegen,S.,
 Verhoeven,T. and Denyer,K.
 TITLE Starch granule initiation and growth are altered in barley mutants
 that lack isomylase activity
 JOURNAL Plant J. 31 (1), 97-112 (2002)
 MEDLINE 22096154
 PubMed 12100486
 REFERENCE 2 (bases 1 to 2445)
 AUTHORS Burton,R.A., Denyer,K. and Fincher,G.B.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-2002) Plant Science, University of Adelaide,
 Waite Campus, Urrbrae, SA 5064, Australia
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 EGDPLRYPKDLVIYEMHFGTKHDSNVHPGTFIGAVSKLDYLKELGVNCILM
 PCHEFNLEVATSSKNFWGYSITNFFSPMTRVTSGGIKNCGRDGINKETFRVESH
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 therefore mis-spliced from the mRNA"

ORIGIN

Alignment Scores:
 Pred. No.: 0 Length: 2445
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 Best Local Similarity: 91.88% Mismatches: 21
 Query Match: 94.69% Indels: 25
 DB: 8 Gaps: 2

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 Qy 22 GluValCysAlaAlaValAlaGluAlaAlaThrLysVal--GluAspGluGlyGluGlu 40
 Db 139 GAGGTCTCGCGCGCGCGCTCGAGCGCGGACGAGCCGAGGAGGAGGAGGAGGAG 198
 Qy 41 AspGluProValAlaGluAspArgTrpAlaLeuGlyGlyAlaCysArgValLeuAlaGly 60
 Db 199 GAGGAGCGCGTGGCTGAGGACAGGTATGCGTCGAGGCGCGTCGACGGTGTCTCGCGGA 258
 Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80
 Db 259 ATGCCCGCGCGCTGGGCGGCCCGCTCGCGCGCGGGTCAATTCGCGCTTACTCA 318

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Db	319	GGCGAGACCGCGCGCTCGCGCTCTCGCCTCTTCAAGCAGAAAGATCTCAAGCGCGATAGG	378
Qy	101	ValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisVal	120
Db	379	GTGAGGAGGAGGTTCCTCTTGACCCCTTGATCGATCGAGCTGGGAGCTGTGGCATGTC	438
Qy	121	PhelLeGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAla	140
Db	439	TTCTCTCGAAGCGAGCTCGACGGCATGCTTTATGGGTACAGGTTTCGACGCGACCTCGCT	498
Qy	141	ProHisCysGlyHisTyrLeuAspValSerAsnValValValAspProTyrAlaLysAla	160
Db	499	CCTCACTCGGCGACTCTTGATGTTTCCAAATGTTGGTGGATGCTTTATGCTTAAGGCA	558
Qy	161	ValLeSerArgGlyGlyTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMet	180
Db	559	GTGATAAGCGGAGGAGTATGTTGTTCCGGCGCATGTTAAACAATTCGTGGCCTCAGATG	618
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Qy	201	TyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAsp	220
Db	679	TATCTCAAAAGGACCTTGTAATATATGAGATGCACCTGCGTGGATTCACGAGCATGAT	738
Qy	221	SerSerAsnValGluHisProGlyThrPhelLeGlyAlaValSerLysLeuAspTyrLeu	240
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Db	799	AAGGAGCTTGGAGTTAATTGTATAGAATTAATGCTCCCTGCCATGAGTTCAACGAGCTGGAG	858
Qy	261	TyrSerThrSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSer	280
Db	859	TATGCAACCTCTCTTCCAAAGATGAACCTTTTGGGGATATTCTACATAAACTCTCTTTCA	918
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Qy	341	AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly	360
Db	1099	AATACTACATACTATATGTTCCACCAAGGAGAGTTTATATACTATTCTGGCTGTGGG	1158
Qy	361	AsnThrPheAsnCysAsnHisProValValArgGlnPheLeValAspCysLeuArgTyr	380
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Qy	401	GlySer-----	402
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Db	1459	AATGACCAAAATCTTGGAGGCGTCAAGCTCATTTGCTGAAGCATGGGATGAGGAGGCGTC	1518
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Qy	517	PheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyr	536
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Qy	537	AsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTirpAsnCys	556
Db	1759	AAATTTACAAATGGGGAGAACACACAGAGATCGAGAAATCACAACTCTTAGCTGGAACTGT	1818
Qy	557	GlyGluGluGlyGluPheAlaArgLeuSerValIysArgLeuArgLysArgGlnMetArg	576
Db	1819	GGGAGGAGAGGAATTCGCAAGATCGTCAAGTCTCAAGATTGAGAGAGGCGAGATGCGC	1878
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Qy	617	PheArgTirpAspLysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThr	636
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Db	2059	AAATTCGCAAGGAGTCGAGGGGCTTGGCCCTTGAGACCTTCCCAACGGCCGAAACACTG	2118
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RESULT 11
AB015615

LOCUS AB015615 2288 bp mRNA linear PLN 06-JUL-2001
 DEFINITION Oryza sativa mRNA for isoamylase, partial cds.
 ACCESSION AB015615
 VERSION AB015615.1 GI:3252793
 KEYWORDS isoamylase.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS Fujita, N., Kubo, A., Francisco, P. B. Jr., Nakakita, M., Harada, K.,
 Minaka, N. and Nakamura, Y.
 TITLE Purification, characterization, and cDNA structure of isoamylase
 from developing endosperm of rice
 JOURNAL Planta 208 (2), 283-293 (1999)
 MEDLINE 99266133
 PUBMED 10333591
 REFERENCE 2 (bases 1 to 2288)
 AUTHORS Nakamura, Y.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-1998) Yasunori Nakamura, National Institute of
 Agrobiological Resources, Department of Plant Physiology, 2-1-2
 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:nakayn@affrc.go.jp, Tel:81-298-38-8382,
 Fax:81-298-38-8347)

FEATURES

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 Best Local Similarity: 89.31% Mismatches: 46
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 DB: 8 Gaps: 0

ORIGIN

Alignment Scores:
 Pred. No.: 1..23e-291 Length: 2288
 Score: 3586.00 Matches: 643
 Percent Similarity: 93.61% Conservative: 31
 Best Local Similarity: 89.31% Mismatches: 46
 Query Match: 85.14% Indels: 1
 DB: 8 Gaps: 0

US-09-674-817B-3 (1-764) x AB015615 (1-2288)

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QY 724 PheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeu 743
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QY 744 TyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgProAsp 763
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RESULT 12

AR427894
LOCUS 2700 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15 from patent US 6639126.
ACCESSION AR427894
VERSION AR427894.1 GI:40186914
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2700)
AUTHORS Sewalt,V.J.H. and Singletary,G.W.
TITLE Production of modified polysaccharides
JOURNAL Patent: US 6639126-A 15 28-OCT-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 3 78e-290 Length: 2700
Score: 3569.50 Matches: 653
Percent Similarity: 90.28% Conservative: 44
Best Local Similarity: 84.59% Mismatches: 65
Query Match: 84.75% Indels: 10
DB: 6 Gaps: 4
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QY 21 yGluVal-----CysAlaAlaValValGluAlaAlaThrLysValG1 35
Db 201 GCGGCTGCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGGA 260
QY 35 uAspGluGlyGluGluAspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCy 55
Db 261 GGCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 320
QY 55 sArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAs 75
Db 321 CCGGCTGCTCGCGGAATGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 380
QY 75 nPheAlaValTyrSerGlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAs 95
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QY 194 uGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuAr 214
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RESULT 14
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LOCUS
DEFINITION
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ACCESSION
U18908
VERSION
U18908.1      GI:758725
KEYWORDS
SOURCE
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2712)
James M.G., Robertson,D.S. and Myers,A.M.
Characterization of the maize gene sugary1, a determinant of starch
composition in kernels
Plant Cell 7 (4), 417-429 (1995)
7773016
2 (bases 1 to 2712)
Myers,A.M.
Direct Submission
Submitted (19-DEC-1994) Alan M. Myers, Biochemistry and Biophysics,
Iowa State University, 2110 Molecular Biology Building, Ames, IA
50011, USA
On Apr 6, 1995 this sequence version replaced gi:755295.
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La Jolla, CA 92093, USA"
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Score: 3528.50
Percent Similarity: 89.64%
Best Local Similarity: 83.94%
Query Match: 83.77%
Indels: 10
Matches: 648
Conservative: 44
Mismatches: 70

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Qy      434 tIleSerAsnAspProIleLeuGlyGlyValIleLeuAlaGluAlaTrpAspAlaG 454
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Qy      554 pAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValIleArgLeuArgIleArg 574
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RESULT 15
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DEFINITION      Sequence 2 from patent US 6469230.
ACCESSION      AR241384
VERSION        AR241384.1    GI:27287051
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 2706)
AUTHORS      Edwards, E.A., Smith, A.M., Martin, C.R. and Bustos Guillen, R.
TITLE          Starch debranching enzymes
JOURNAL        Patent: US 6469230-A 2 22-OCT-2002;
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Query Match:    71.91%      Indels:      28
DB:             6          Gaps:        7

US-09-674-817B-3 (1-764) x AR241384 (1-2706)
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Db      238 -----GTGAAGACTGCGGCTACTCGGTGTGGTGGAG-----AAGCCG 276
Qy      44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArg-----ValLeuAlaGlyMet 61
Db      277 ACGACGGAA-----CGATGCTGTTTGGAGTTTATCAGGGAAG 315
Qy      62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81
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Qy      82 GlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101
Db      376 AATGTCACAGTGTCTACTCTTTGCTTGTATCATCTTTCCGATTTTCCCTGAGAAAGAGTG 435
Qy      102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPhe 121
Db      436 ACCGAGCAAAATTTTCTGGATCCTCTAGCTAATAAATAACTGGAGATGATGTCATGCTTC 495
Qy      122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141
Db      496 CTTAAGGAGAGATTTTGAAGAATATGCTATATGCTGCTACAAATTTGATGGGAAATTTCTGCTCT 555
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Qy 537 AsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCys 556
Db 1756 AATTGGCAATGGAGAGGACCAACAAAGACGGGAGAAATCACAAATAATAGTTGGAATGT 1815
Qy 557 GlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArg 576
Db 1816 GGTGAGGAAGAGAAATTTGCAAGTATCTTTGTGAAGAAATTTGAGAAAGACAAATGCGG 1875
Qy 577 AsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGlu 596
Db 1876 AACCTCTCTCTGCTTATGGTTTCCCAAGGTGTTCCCATGATATATATGCGCGATGAA 1935
Qy 597 TyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyr 616
Db 1936 TATGTCACACTAAGGAGGAGAAACACACACGATTTGCCATGATATAATATATAATAC 1995
Qy 617 PheArgTrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCysLeuMet 635
Db 1996 TTCGTTGGGATAGAAGGATGAATCTTCATCTGATTTTGGATTTTGGCGCTCATG 2055
Qy 636 ThrLysPheArgLysGlyCysGlyGlyLeuGlyLeuGluAspPheProThrAlaLysArg 655
Db 2056 ACCAAATTCGCCCATGAATGTGAATCACTGGGATTTAGATGTTTCCCTACAGCAGAAAG 2115
Qy 656 LeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheVal 675
Db 2116 CTGCAATGGCATGTCTCACTCTAGAACTCCAGATTGGTCTGAAACAAGTCGATTCGTT 2175
Qy 676 AlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHis 695
Db 2176 GCATTCACACTGGTCGACAAAGTGAAGGAGAACTATATATGCTTTAAACGCCAGCCAT 2235
Qy 696 LeuProAlaValValGluLeuProGluArgAlaGlyArgTrpGluProValValAsp 715
Db 2236 TTGCTGTAAAGATTACACTTCCAGATAGGCTGGTTATAGATGGCAGCCGTTTGGAC 2295
Qy 716 ThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThr 735
Db 2296 ACAGCAACACAGCAGCACCATTGACTTCTTGACAGACGACGCTTCTGAGAGAGACAGCA 2355
Qy 736 IleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSer 755
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Qy 756 ValIleLeuValLeu 760
Db 2416 ATTATCTTTTACTA 2430

Search completed: August 10, 2004, 03:42:27
Job time : 7766 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 9, 2004, 22:04:15 ; Search time 728 Seconds

(without alignments)
4458.274 Million cell updates/sec

Title: US-09-674-817B-3

Perfect score: 4212
Sequence: 1 SGAPLRWRPNATAGKV.....SNLYPMLSYSSVILVLRDPV 764

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_29Jan04.*
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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4050	96.2	2997	3	Aaz24492 Wheat iso
2	3528.5	83.8	2712	2	Aax76375 Zea mays
3	3528.5	83.8	2712	6	Aad47816 Alternati
4	3515.5	83.5	2715	6	Aad42890 Maize sug
5	3029	71.9	2706	2	Aax27061 S. tubero
6	2923	69.4	2806	2	Aax27066 Original
7	2918	69.3	1706	2	Aax34654 Partial c
8	2855.5	68.7	2352	6	Abz12413 Arabidops

9	2895.5	68.7	2352	7	ADA67900	Ada67900 Arabidops
10	2612	62.0	2133	2	AAT96754	Aat96754 S. tubero
11	2359.5	56.0	9289	2	AAX34655	Aax34655 Hexaploid
12	2234	53.0	11779	6	AAD42891	Aad42891 Maize sug
13	2179	51.7	10439	6	AAD47817	Aad47817 Alternati
14	1884	44.7	1663	2	AAX33162	Aax33162 Potato is
15	1577	37.4	2634	2	AAX27062	Aax27062 S. tubero
16	1487	35.3	2370	7	ADA71085	Ada71085 Rice gene
17	1379	32.7	4745	6	ABS54601	Ab54601 Synechoco
18	1305.5	31.0	1995	6	ABL92608	Ab192608 Chlamydia
19	1305.5	31.0	1995	7	ACA30742	Aca30742 Prokaryot
20	1305.5	31.0	110000	2	AXX91990_04	Continuation (5 of
21	1305.5	31.0	273254	3	AXC81914	Axc81914 Chlamydia
22	1300	30.9	1998	6	ABL92637	Ab192637 Chlamydia
23	1266.5	30.1	110000	2	AAX01425_04	Continuation (5 of
24	1264	30.0	2001	7	ACA31084	Aca31084 Prokaryot
25	1225.5	29.1	349980	6	ABQ81846	Abq81846 Bifidobac
26	1225	29.1	110000	4	AAI99682_17	Continuation (18 o
27	1225	29.1	110000	4	AAI99683_17	Continuation (18 o
28	1204	28.6	2508	5	AAH67270	Aah67270 C Glutami
29	1204	28.6	349980	5	AAH68531	Aah68531 C Glutami
30	1187	28.2	2181	2	AAZ07446	Aaz07446 Rhodothe
31	1187	28.2	2181	3	AAZ89961	Aaz89961 Isoamylas
32	1149.5	27.3	2151	7	ABT14630	Abt14630 Pseudomon
33	1062.5	25.2	22934	4	AA559613	Aa559613 Propionib
34	1062.5	25.2	22934	7	ACF64542	Acf64542 Propionib
35	1032.5	24.5	1389	2	AAZ27067	Aaz27067 Original
36	1014	24.1	1980	7	ACA34446	Aca34446 Prokaryot
37	1014	24.1	110000	2	AAT42063_14	Continuation (15 o
38	996	23.6	1989	7	ACA42966	Aca42966 Prokaryot
39	980.5	23.3	1965	4	AA556077	Aa556077 Salmonell
40	971	23.1	1913	4	AA771541	Aaf771541 Corynebac
41	915.5	21.7	2843	2	AAZ27060	Aaz27060 S. tubero
42	910.5	21.6	2843	2	AAZ27065	Aaz27065 Original
43	890	21.1	2649	6	ABZ12474	Abz12474 Arabidops
44	830.5	19.7	603	9	ADC08661	Adc08661 Wheat DNA
45	825	19.6	2325	2	AAT95400	Aat95400 Flavobact

ALIGNMENTS

RESULT 1

AAZ24492

ID AAZ24492 standard; DNA; 2997 BP.

XX

AC AAZ24492;

XX

DT 18-FEB-2000 (first entry)

XX

DE Wheat isoamylase cDNA.

XX

KW Isoamylase; wheat; transgenic plant; starch production; food; baking;
KW pastry; packaging material; glucose; glucan; paper; pulp; adhesive;
KW textile building material; soil stabilizer; wetting agent; fertilizer;
KW plant-protection; cosmetic; flocculant; ss.

XX

OS Triticum aestivum.

XX

PH Location/Qualifiers

FT CDS

FT 1..2924

FT /*tag= a

FT /product= "isoamylase"

FT /codon start= 3

FT /note= "coding sequence is interrupted by introns and the

FT start codon is not disclosed"

FT 1..295

FT /*tag= b

FT /number= 1

FT 296..395

FT /*tag= c

FT /number= 1

FT 396..1616

FT /*tag= d

FT exon

FT intron

FT exon

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FT intron /number= 2
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FT /number= 2
FT 2135..2924
FT /*tag= f
FT /number= 3
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XX DE19820608-AL.
XX
XX 11-NOV-1999.
XX
XX 08-MAY-1998; 98DE-01020608.
XX
XX 08-MAY-1998; 98DE-01020608.
XX (AGRE ) HOECHST-SCHERING AGREVO GMBH.
XX
XX Loerz H, Luetticke S, Abel G;
XX
XX WPI; 2000-024509/03.
XX
XX P-PSDB; AAY50819.
XX
XX New nucleic acid encoding isoamylase from wheat and related transgenic
XX plants producing starch with altered properties.
XX
XX Claim 1b; Page 14-15; 18pp; German.
XX
XX This invention describes a novel wheat isoamylase. Transgenic plants,
XX specifically wheat, that contain (1) are used for production of starch,
XX used particularly in foods, particularly baked and pastry goods and for
XX making packaging materials or disposable items. Starch may also be used
XX as starting materials for glucose or glucan components (e.g. for
XX fermentation or further chemical conversion); in paper and pulp
XX production; as adhesives; in textiles; in preparation of gypsum-based
XX building materials; as soil stabilizer; as wetting agent etc. in
XX fertilizer and plant-protection compositions; as binder (in
XX pharmaceuticals, cosmetics, coal briquetting and casting sand); as
XX flocculant in soil or coal slurries; as rubber and leather additives; and
XX for production of synthetic polymers, e.g. polyurethane films. Transgenic
XX plants with increased/decreased production of (1) produce starches with
XX altered physical and/or chemical properties, e.g. amylose/amylopectin
XX ratios; degree of branching; mean chain length; phosphate content;
XX gelatinization properties; gel- or film-forming properties, or starch
XX grain size or structure, e.g. easier, and less expensive, digestion by
XX enzymes. This sequence encodes the wheat isoamylase protein described in
XX the invention
XX
XX Sequence 2997 BP; 803 A; 636 C; 762 G; 796 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 2997
Score: 4050.00 Matches: 763
Percent Similarity: 78.34% Conservative: 0
Best Local Similarity: 78.34% Mismatches: 1
Query Match: 96.15% Indels: 211
DB: 3 Gaps: 2
US-09-674-817B-3 (1-764) x AA224492 (1-2997)
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QY 21 GlyGluValCysAlaAlaValAlaValGluAlaAlaThrLysValGluAspGluGluGlu 40
Db 63 GGCAGAGTGTGCGCGCGGTGTGCGAGCGCGGACGAGGTAGACGACGAGGGGAGGAG 122
QY 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGly 60
Db 123 GACGAGCGGTGGCGGAGGACAGGTACGCGCTCGGGCGGGCGGGCGGGCGGGCGGGCGGA 182
QY 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80

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Db 183 ATGCCCGCGCGCTGGGGCGCCACCGCGCTCGCCGGGGGTCAATTTCCGGCGTCTATTCC 242
QY 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97
Db 243 GCGGAGCCACCGCGCGGGGCTCTGCTCTTTCACGCCAGAAGATCTCAAGGGGTTGGGG 302
QY 97 ----- 97
Db 303 TTGCTCCCGAGTAGAGTTTCATCAGCTTTCGTCGCGCGCGCCCTTTTTCGGGCTG 362
QY 98 -----Ala-AspArgValThrGluGluValProLe 107
Db 363 CAATTTAAGTTTGTACTGGGGCAATGCTGCAGATAGGGTAGCCGAGGAGTTTCCCT 422
QY 107 uAspProLeuMetAsnArgThrGlyAsnValTTPHisValPheIleGluGluLeuHi 127
Db 423 TGACCCCTGATGAATCGGACCGGAAACGTGTGGCATGTCTTCATCGAAGCGGAGCTGCA 482
QY 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe 147
Db 483 CAACATGCTTTACGGGTACAGTTTCGACGGCACCTTTGCTCCTCCTGCGGGCAGCTACCT 542
QY 147 uAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyr 167
Db 543 TGATGTTTCCAATGCTGTTGGTGGATCCTTATGTAAGGCAGTGATAAGCCGAGGGAGTA 602
QY 167 rGlyValProAlaArgGlyAsnAsnCysTTPProGlnMetAlaGlyMetIleProLeuPr 187
Db 603 TGGTGTTCACGCGGTGGTAACAATGCTGCGCTCAGATGGCTGGCATGATCCCTCTTCC 662
QY 187 oTyrSerThrPheAspTTPGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuVa 207
Db 663 ATATAGCACGTTTGAATTGGGAAGCGCACCTACCTCTAAGATATCTCTCAAAAGGACCTGGT 722
QY 207 lIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227
Db 723 AATATATGAGATGACCTTGGCGTGGATTTCAGAGCATGATTCAGCAATATAGAACATCC 782
QY 227 oGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCy 247
Db 783 GGGTACTTTTCATTGGAGCTGTTCGAGCTTGACTATTTCAGGAGCTTGGAGTTAATTG 842
QY 247 sIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerLys 267
Db 843 TATTGAATTAATGCGCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCAA 902
QY 267 sMetAsnPheTTPGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSe 287
Db 903 GATGAACCTTTTGGGGATATTCTACCAATAAACTCTTTTCCAAATGACCAAGATACATC 962
QY 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgG 307
Db 963 AGCGGGATATAAAACTGTGGCGGTGATGCCATAAATGAGTTCAAAACTTTTGTAAAGA 1022
QY 307 uAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGlu 327
Db 1023 GGCTCACAAACGGGGAATTGAGGTGATCCCTGGATGTTGTCTTCAACCATACAGCTGAGG 1082
QY 327 yAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLe 347
Db 1083 TAATGAGATGTTCCATATATATCATTTAAGGGGTGATAATACTACATCTATATGCT 1142
QY 347 uAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHi 367
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QY 367 sProValValArgGlnPheIleValAspCysLeuArgTyrTTPValThrGluMetHisVa 387
Db 1203 TCCTGTGGTTCGTCAATTCTATTAGATTGTTTAAAGATCTGGGTGACGGAATGCATGT 1262
QY 387 lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTTPAspPr 407

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 Db 1323 AGTTAACGTGTATGGAGCTCAATAGAGGTGACATGATCACACAGGACACCTCTTGT 1382
 Qy 427 lThrProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIysLeuI 447
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 Qy 447 eAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnVa 467
 Db 1443 TGCTGAAGCATGGGATCAGAGGCTCTATCAAGTAGGTCAATTCCTCACTTGGAAATGT 1502
 Qy 467 lTrpSerGluTrpAsnGlyIysTyrArgAspIleValatGlnPheIleIysGlyThrAs 487
 Db 1503 TTGCTGTAGTGAATGGAGTACCGGACATTTGCGTCAATTCATTAAAGGCACTGA 1562
 Qy 487 pGlyPheAlaGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAla-- 506
 Db 1563 TGGATTTGCTGTGGTGTTCGCCGAATGCTCTTTGTGGAAGTCCACACTATACCAGT-AA 1621
 Qy 506 ----- 506
 Db 1622 GTTGTGCCAATCTGTAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATACCA 1681
 Qy 506 ----- 506
 Db 1682 CATGATGATACACATCTAAATATATAACAAATCATAGTGTATGATATGCAATTTGGCTAAG 1741
 Qy 506 ----- 506
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 Qy 506 ----- 506
 Db 1862 CCAGCCATGTCAATTTTTAGGGGGGAGAGAACTATATTGATTTGCCCTCCCTAAAGA 1921
 Qy 506 ----- 506
 Db 1922 AGCAATCTCAGAAATTCATAGTAAGTTGCTTTCTGTAAAGAAAGAAACGACTCATTA 1981
 Qy 506 ----- 506
 Db 1982 CTTTCTATCGGTGCTAACTTAGCTCGATGTATATTGTAAGATGAATGCCAAATTTAAT 2041
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 Db 2042 TGTGGGAATTTGATCTGTTATTTCAAAATTTCTATTGTTTCTCTAGAAATCAAAAC 2101
 Qy 507 ----- GlyValArgIysPr 511
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 Db 2222 ATATAATAAGAGTACAAATTTACAAATGGGAGAGAACACAGAGATGGAGAAATCACAA 2281
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 Db 2342 GAAGAGGCAGATGCCAAATTTCTTTGTTTGTCTCATGGTTTCTCAAGGAGTTTCCAATGTT 2401

Qy 591 eTyrMetGlyAspGluTyrGlyHisThrIysGlyGlyAsnAsnAsnThrTyrCysHisAs 611
 Db 2402 CTCATGGTGTATGATGATATGGCCACACAAAAGGGGGCAACCAACATACATACTGCCATGA 2461
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 Db 2462 TTCCTTATGTCAATTTTTCGCTGGATATAAAGAACAAATACCTGAGTTGCACCGATT 2521
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 Qy 651 cThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAs 671
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 Qy 751 uSerTyrSerSerValIleLeuValLeuArgProAspVal 764
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RESULT 2

AAX76375
 ID AAX76375 standard; cDNA; 2712 BP.

AC AAX76375;

DT 04-AUG-1999 (first entry)

ZE Zea mays SU1 starch debranching enzyme encoding cDNA clone.

ZE Zea mays; SU1; starch debranching enzyme; maize; endosperm; corn;
 KW bacterial isoamylase; alpha-amylase; starch hydrolytic enzyme; sugary 1;
 KW SS.

OS Zea mays.

FH Key Location/Qualifiers
 FT 1..2457
 FT /*tag= a

PN US912413-A.

PP 15-JUN-1999.

PP 24-MAR-1995; 95US-00410784.

PP 24-MAR-1995; 95US-00410784.

PA (IOWA) UNIV IOWA STATE RES FOUND INC.

PI Myers AM, James MG;

PI WPI; 1999-357234/30.

DR P-PSDB; AAY17523.

PT SU1 starch debranching enzyme.

QY 594 lYaspGluTyrGlyHisThrLysGlyGlyAsnAsnThrThrCysHisAspSerTyrV 614
 Db 1943 GCGATGAATATGGFCACACAAAGGGAGGGAACAAATACGTACTCCCATGACCATATG 2002
 QY 614 aLAsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysC 633
 Db 2003 TCATATATTCCTGGATAGAGGAAGAAACAATCCCTGATTTGTACAGATTCGCG 2062
 QY 633 ysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThra 653
 Db 2063 GTCTCATGACGCAATCCGCAAGAATGTGAATCTCTTGGCCCTTGAGGACTTCCGCACT 2122
 QY 653 lAlAsnTyrLeuGlnTrpPheGlyHisGlnProGlyLysProAspTyrSerGluAsnSera 673
 Db 2123 CAGAACGGTGAATGACGCGTCAATCAGCCCGGAGCGCTGACTGTAGAGGCAAGCC 2182
 QY 673 rgPheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnT 693
 Db 2183 GATTCGTGCTTCACCATGAAGACGAAACCAAGCGAGATCTACGTGGCCTTCAACA 2242
 QY 693 hrSerHisLeuProAlaValAlaValLeuProGluArgAlaGlyArgTyrProGluProV 713
 Db 2243 CCAGTCACCTTCGCGTGGTGTGGGCTTCCAGAGCGCTTGGGTTCCGATGGGAGCGG 2302
 QY 713 alValAspThrGlyLysProAlaProLysPheLeuThrAspPheLeuProAspArgA 733
 Db 2303 TGGTGGACACCGCAAGGAGGACCATATGACTTCTCACCAGATGCGCTGCCAGATCGTG 2362
 QY 733 laLeuThrLeHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerT 753
 Db 2363 CTGTACCGCTACCGAGTCTCTCTATTCTCCTCAACTCCAATCTCTATCTATGCTCAGT 2422
 QY 753 yrSerSerValIleLeuValLeuArgProAspVal 764
 Db 2423 ACTCCTCATCATCTCTGATTGGCCCTGATGTC 2457

RESULT 5
 AAX27061
 ID AAX27061 standard; DNA; 2706 BP.
 XX
 AC AAX27061;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE S. tuberosum isoamylase clone 15 coding sequence.
 XX
 KW Isoamylase clone; potato; branched polysaccharide synthesis; amylopectin;
 KW starch modification; debranching activity; ss.
 XX
 OS Solanum tuberosum.
 XX
 PN WO9906575-A1.
 XX
 PD 11-FEB-1999.
 XX
 PF 30-JUL-1998; 98WO-GB002280.
 XX
 PR 31-JUL-1997; 97GB-00016185.
 XX
 PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX
 PI Edwards EA, Smith AM, Martin CE, Bustos Guillen R;
 XX
 DR WPI; 1999-153803/13.
 DR P-PSDB; AAY00869.
 XX
 PT New nucleic acid from potato encoding starch debranching enzyme with
 PT isoamylase activity - and related vectors, transformed cells and plants,
 PT proteins and antibodies, used to generate starch with altered properties,
 PT for use in foods, as thickeners etc.
 XX
 PS Claim 3; Fig 2; 78pp; English.

XX
 CC This sequence encodes a Solanum tuberosum isoamylase of the invention.
 CC Fragments of the isoamylase coding sequence are used to identify and
 CC clone isoamylases from other plant species, by standard hybridisation or
 CC amplification methods. Expression of the isoamylase DNA in host cells is
 CC used to produce the isoamylase which is used: (i) to raise antibodies
 CC (Ab) for identification, isolation and localisation of isoamylases; and
 CC (ii) for synthesis of branched polysaccharides. The DNA, proteins and Ab
 CC (or related peptides) are used to alter the quality and quantity of
 CC polysaccharides in a host cells, specifically to alter branching in
 CC amylopectin. The modified starches produced are useful in human or animal
 CC foods; as biodegradable plastic; as food or paint thickener; in starch-
 CC coated films, paper and textiles; in mining explosives; in
 CC pharmaceuticals and glues. Manipulation of debranching activity in a
 CC plant allows control of starch properties, e.g. increased gel strength;
 CC formation of paste rather than gel, changed physical characteristics etc
 XX

SQ Sequence 2706 BP; 797 A; 492 C; 624 G; 792 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 6,54e-279 Length: 2706
 Score: 3029.00 Matches: 546
 Percent Similarity: 81.57% Conservative: 78
 Best Local Similarity: 71.37% Mismatches: 113
 Query Match: 71.91% Indels: 28
 DB: 2 Gaps: 7

US-09-674-817B-3 (1-764) x AAX27061 (1-2706)

QY 10 TrpArgPro-----AsnAlaThrAlaGlyLysGlyValGlyGluVal 23
 Db 178 TGGAGAAAATCGAGGTCTTCAGTGGTTAAATGCTGCTGCTGATGACGTGGAGTGTG 237
 QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluGluAspGluPro 43
 Db 238 -----GTGAAGACTGGCGTACTGCGGTGGTGGTGAG-----AAGCCG 276
 QY 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArg-----ValLeuAlaGlyMet 61
 Db 277 ACGACGGAA-----CGATGTCGTTTGGAGGTTTATCAGGGAAG 315
 QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81
 Db 316 CCATGCGGTTTGGTGTCTACTGCGACAGATGGTGTGAAATTCGCTGTTTTCAGG 375
 QY 82 GlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101
 Db 376 AATGCTACAGCTGTACTCTTTGCTTGCATCCTCTTCCGATTACCTGAGAAGAGAGTG 435
 QY 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyrHisValPhe 121
 Db 436 ACCAGCAAAATTTTCCGGATCTCTAGCTAAATAAACTGGAGATGTATGCGATGTGTC 495
 QY 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141
 Db 496 CTTAAGGGAGATTTTGAGATATGCTATATGCTACAAATTCATGGAAATCTGTCTCT 555
 QY 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161
 Db 556 GAAGAAGGACACTACTTTGACTCTTCGACAGATAGTGTGGATCTTATGCAAGGTATA 615
 QY 162 IleSerArgGlyGluTyrGlyValProAlaArgValAsnAsnCysTyrProGlnMetAla 181
 Db 616 GTAACGACGAGGAGATATGTTGTTATAGGCCACAGAGATGTTGTTGCCCAATGGCT 675
 QY 182 GlyMetIleProLeuProTyrSerThrPheAspTyrGlyAspLeuProLeuArgTyr 201
 Db 676 GGCATGTGCTCTGCTTCTGCTTCTGATCAGTTTGAATGGAGAGAGATCTTACCACTGAAGTT 735
 QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSer 221
 Db 736 CCACGAGAGATCTTGAATGAAATGCAATGTTGCTGGGTTTACTAATCATGAGTCG 795

XX Disclosure; Fig 11; 7app; English.

XX This sequence represents the original isolated clone encoding a Solanum
 CC tuberosum isomylase of the invention. Fragments of the isomylase coding
 CC sequence are used to identify and clone isomylases from other plant
 CC species, by standard hybridisation or amplification methods. Expression
 CC of the isomylase DNA in host cells is used to produce the isomylase
 CC which is used: (i) to raise antibodies (Ab) (for identification,
 CC isolation and localisation of isomylases); and (ii) for synthesis of
 CC branched polysaccharides. The DNA, proteins and Ab (or related peptides)
 CC are used to alter the quality and quantity of polysaccharides in a host
 CC cells, specifically to alter branching in amylopectin. The modified
 CC starches produced are useful in human or animal foods; as biodegradable
 CC plastic; as food or paint thickener; in starch-coated films, paper and
 CC textiles; in mining explosives; in pharmaceuticals and glues.
 CC Manipulation of debranching activity in a plant allows control of starch
 CC properties, e.g. increased gel strength; formation of paste rather than
 CC gel, changed physical characteristics etc

XX Sequence 2806 BP; 818 A; 523 C; 654 G; 807 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.: 9,31e-269 Length: 2806
 Score: 2923.00 Matches: 538
 Percent Similarity: 80.23% Conservative: 79
 Best Local Similarity: 69.96% Mismatches: 119
 Query Match: 69.40% Indels: 33
 DB: 2 Gaps: 9

US-09-674-817B-3 (1-764) x AAX27066 (1-2806)

Qy 10 TrpArgPro-----AsnAlaThrAlaGlyLysGlyValGluVal 23

Db 241 TGGAGAAATCGAGGCTTCAGTGGTTAATGCTGCTTGTATAGTGCAGCTGGAGGTG 300

Qy 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGluAspGluPro 43

Db 301 -----GTGAAGACTGGCGGTACTGCGGTGGTGGAG-----AAGCCG 339

Qy 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgVal-----LeuAlaGlyMet 61

Db 340 ACGACGAA-----CGATGTCGTTGAGGTTTTCAGGGAAAG 378

Qy 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81

Db 379 CCATTCGCGTTGCTGCTACTGCGACAGATGGTGGTGAATTCGCTGTTTTCAGGA 438

Qy 82 GlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101

Db 439 AATGCTACAGCTGCTACTCTTCTGCTGATCATCTCTTCCGATTTACTGAGAGAGGTG 498

Qy 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPhe 121

Db 499 ACCGAGCAAAATTTCTCGGATCCTCTAGCTAATAAATACTCGAGATGTATGGCATGTGTTTC 558

Qy 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141

Db 559 CTTAAGGGAGATTTTGAGATAATGCTATATGGCTACAAATTTGATGGAAATTCGTCTCT 618

Qy 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161

Db 619 GAAGAAGGACACTACTTTGACTCTTCGACATAGTGTGGATCTTATGCCAAGGCTATA 678

Qy 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAla 181

Db 679 GTAAGCAGAGAGAATAATGTTGATTAGGGCCAGAGGATGATTGTCGCCCAATGGCT 738

Qy 182 GlyMetIleProLeuProTyr---SerThrPheAspTyrGluGlyAspLeuProLeuArg 200

Db 739 GGCATGGTACCCCTCTGCTTCGATCATGTTGATTTGGAGGAGAGATCTACCACTGGAA 798

Qy 201 --TyrProGlnLysAspLeuVal-IleTyrGluMetHisLeuArgGlyPheThrLysHis 219

Db 799 GTTCCACACAGAGATCTTGTNATCNATGAATGCATGTTCTGCTGGTTTACTATCCAT 858

Qy 220 AspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyr 239

Db 859 GAGTCGAGTGAACAACAATAATCTCGTACTTACCTGGTGTGGGAGAACTTGATCAC 918

Qy 240 LeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeu 259

Db 919 TTGAAGAGACTTGGTGTCAACTGTATAGAGCTATGCCCTGTACAGAGTTCATGAGCTG 978

Qy 260 GluTyrSerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSer 274

Db 979 GAGTACTATATTTAATCTGTATTTGGCGACACAAAGTTTAACTTTTGGGGCTATCT 1038

Qy 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294

Db 1039 ACTGTCAATTTCTTTCTCCAAATGGGAGATACTCATCTGCTGCTCTAAGTAATTTGGCG 1098

Qy 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314

Db 1099 CTCGGTGCATATAACGAATTTAAGTATCTTGTCAAGCAAGCACATAAACCGTGAATCGAG 1158

Qy 315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334

Db 1159 GTTATCATGGATGTTGTTTTCATACACACTGCTGAAGAAATGAAATGGTCCCATACTA 1218

Qy 335 SerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr 354

Db 1219 TCATTTAGAGCAATGACACAGTGTGTTTATACGCTAGCTCTCTAAGGTTGAATTTTAC 1278

Qy 355 AsnTyrSerGlyCysGlyAsnThrPheAsnHisProValValArgGlnPheIle 374

Db 1279 AACTACTCAGATGTGGAATACCTTCAACTGTAATATCCATTTGACGTCAATTTATA 1338

Qy 375 ValAspCysLeuAspTyrTyrValThrGluMetHisValAspGlyPheArgPheAspLeu 394

Db 1339 GTG---ATGCTGAGATATGGTTTACCGAATGACAGTACATGGCTTCCGCTTGATCTT 1395

Qy 395 AlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPro 414

Db 1396 GCTTCTATCTCTTACAAGAAGTAGCAGCTCGTGAATGCTGTAAATGCTCTATGAAATTC 1455

Qy 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMet 434

Db 1456 ATTGACGTGACGTGATCACACAGGACCTCTCTCAAGCCACCATTTGATGATG 1515

Qy 435 IleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly 454

Db 1516 ATTAGCAATGATCCAACTACTTCGTGGAGTAAAGCTTATAGCTGAAGCATGGGATTGTGA 1575

Qy 455 GlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474

Db 1576 GGCCTTTACCAAGTTGGCATGTTTCCGCACCTGGGGTATCTGTCGGAGTGAACGGAAG 1635

Qy 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAla 494

Db 1636 TACCGTGACATGGTACGGCAGTTCATCAAGGCATCTGATGGTTTCTGGGGCTTTTGTCT 1695

Qy 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSer 514

Db 1696 GAATGCTCTTGTGAAGCCCAATCTATACAGAAAGGAGAGAAACCATGGAACAGT 1755

Qy 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534

Db 1756 ATAAATTCGTGTGTGCCAGATGGTTTACTTTGGCTGATTTAGTGACATACACAAT 1815

Qy 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp 554

Db 1816 AAACACAATTTGGCAATTTGGAGAGGACAAACAAAGCGGGAGATCAACAATAATAGTGG 1875

Qy 555 AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuAspGlyArgGln 574

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Db 1876 AATTGTCGTGAGGAGAGAAATTTGCAAGTATCTTTGTGAAGAAATGAGGAAAAACACAA 1935
Qy 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
Db 1936 ATGCGGAACCTCTTCCTCTGCTTATGTTTCCCAAGGTGTTCCCATGATATATATGGGC 1995
Qy 595 AspGluTyrGlyHisThrLysGlyValAsnAsnThrTyrCysHisAspSerTyrVal 614
Db 1996 GATGAATATGTCACATTAAGGGAGGAAACAAACACACGTTATGCGCATGATAATATAT 2055
Qy 615 AsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633
Db 2056 AATTACTTCGTTGGGATAAGAGGATGAATCTTCATCTGATTTTGGAGATTTGGCGC 2115
Qy 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 653
Db 2116 CTCATGACCAAAATTCGCCCATGAATGAATCACTGGGATTAGATGTTTCCCTACAGCA 2175
Qy 654 LysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArg 673
Db 2176 GAAAGGCTGCAATGGCATGGTCACACTCTTAGACTCCAGATTGGTCTGAACAAGTCGA 2235
Qy 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThr 693
Db 2236 TTCGTTGCATTCACACTGGTCGACAAAGTGAAGGGAGAACTATATATTTGCTTTAACGCC 2295
Qy 694 SerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgArgTyrGluProVal 713
Db 2296 AGCATTTGCTGTAAACATTACACTTCCAGATAGGCTGGTATAGATGGCAGCGTTT 2355
Qy 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733
Db 2356 GTGCACACAGCAAAACCCAGCACCATTTGACTTCTTGACACGACGCTTCCTGAGAGAG 2415
Qy 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753
Db 2416 ACAGACGCCAAACAATATTTCTCAATTTCTGGACGCGAACCAGTATCCGATGCTCAGTAT 2475
Qy 754 SerSerValIleLeuValLeu 760
Db 2476 TCATCCATTATCTTTTACTA 2496

RESULT 7
AAX34654
ID AAX34654 standard; cDNA; 1706 BP.
XX
AC AAX34654;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Partial cDNA for hexaploid wheat DBE.
XX
KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isomylase; glycogen synthase;
KW wSBE I-D4 gene; ss.
XX
OS Aegilops tauschii.
XX
PH Key Location/Qualifiers
FT CDS 1..1704
FT /tag= a
FT /note= "partial DBE; the att and stop codons are not
FT indicated"
XX
PN W09914314-A1.
XX
PD 25-MAR-1999.
XX
PF 11-SEP-1998; 98WO-AU0000743.
XX

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PR 12-SEP-1997; 97AU-00009108.
PR 20-MAR-1998; 98AU-00002509.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU ) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI Li Z, Morell M, Rahman S;
XX
DR WPI; 1999-229525/19.
DR P-PSDB; AAY06918.
XX
PT New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisense sequences of granule bound synthase.
XX
PS Claim 47; Page 100-102; 171pp; English.
XX
CC The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC rice or maize. The methods and products can be used for targeting
CC expression specifically to the endosperm of the seeds of cereal plants
CC such as wheat or barley. They can be used for the expression of e.g.
CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.
CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial
CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
CC used for modifying the characteristics of starch produced by a plant. The
CC present sequence represents the wheat DBE partial cDNA sequence. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1706 BP; 467 A; 355 C; 415 G; 469 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.37e-268 Length: 1706
Score: 2918.00 Matches: 525
Percent Similarity: 99.25% Conservative: 3
Best Local Similarity: 98.68% Mismatches: 4
Query Match: 69.28% Indels: 0
DB: 2 Gaps: 0

US-09-674-817B-3 (1-764) x AAX34654 (1-1706)

Qy 233 AlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetPro 252
Db 1 GCTGTGTCGAGCTTGACTATTGAGGAGCTTGAGTAAATTGATTGAAATTAATGCC 60
Qy 253 CysHisGluPheAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheTyrGly 272
Db 61 TGCCATGAGTTCACGAGCTGGAGTACTCAACCTCTTCCAGATGAACCTTTTGGGGA 120
Qy 273 TyrSerThrIleAsnPheSerProMetThrArgTyrThrSerGlyIleLysAsn 292
Db 121 TATTTCCATTAATACTTCTTTCACCATGACGAGATACATCATCAGCGGGGNTAATAAAC 180
Qy 293 CysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGly 312
Db 181 TGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGAGCGCTCACAAACGGGA 240
Qy 313 IleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyPro 332
Db 241 ATTGAGGTGATCTGGATGTTGTTCTTCAACCATACGCTGAGGGTAAAGATGTTCA 300
Qy 333 IleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGlu 352
Db 301 ATATTATCATTTAGGGGGTGTGATAATACTACTATATGCTTGTGACCAAGGAGAG 360
Qy 353 PheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGln 372
Db 361 TTTTATAACTATTCTGGCTGGGGAATACCTTCAACTGATTAATCATCTGTTGTTGCTCAA 420
Qy 373 PheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPhe 392

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Db 421 TTCAATGTTAGATTCTTTAAGATACTGGGTGATGAAATGATGTTGATGGTTTTTCGTTTT 480
Qy 393 AspleualaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGly 412
Db 481 GATCTTCATCCATAAATGACAGAGGTTCAGTCTGGGATCCAGTTAACGGTGTATGGA 540
Qy 413 AlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIle 432
Db 541 GCTCCANTAGAGGTGACATGATCACACAGGACACCTCTTGTACTCCACCACCTATT 600
Qy 433 AspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuIleAlaGluAlaTrpAsp 452
Db 601 GACATGATCAGCAATGACCAATTTCTGGAGGCTCAAGCTCATGCTGAAGCATGGAT 660
Qy 453 AlaGlyGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsn 472
Db 661 GCAGAGGCTCTATCAAGTAGGTCAATTCCTCCTGGAATGTTGGTCTGAGTGAAT 720
Qy 473 GlyLysTyrArgAspIleValArgGlnPheIleGlyGlyThrAspGlyPheAlaGlyGly 492
Db 721 GCGAAGTACCGGACATTTGTGGCAATTCATTAAGGCACCTGATGCAATTTGCTGGTGT 780
Qy 493 PheAlaGluCysLeuGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrp 512
Db 781 TTTCCCGAATGCTTTTGTGGAAGTCCACCTATACAGGCGAGGAGGAAACCTTGG 840
Qy 513 HisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyr 532
Db 841 CACAGTATCAACTTTGTATGTGCACATGATGGATTTACACTGGGTGATTTGGTAACAT 900
Qy 533 AsnLysLysTyrAsnLeuProAsnGlyGluAsnArgAspGlyGluAsnHisAsnLeu 552
Db 901 AATAACAAGTACATTTTACCATAATGGGAGAACAAATAGAGATGGAGAAATCAATCTT 960
Qy 553 SerTrpAsnGlyGlyGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLys 572
Db 961 AGCTGGAAATTTGGGGAGGAGGAGAAATTCGACAGATTGTCTCAAAAGATTGAGGAG 1020
Qy 573 ArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyr 592
Db 1021 AGGCAGATGGCGAATTTCTTTGTTGTCTCATGCTTTCTCAAGGAGTTCAATGTTTAC 1080
Qy 593 MetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSer 612
Db 1081 ATGGCGCATGAATATGCCACACAAAGGGGGACAAACAAATACATCTGCGCATGTTT 1140
Qy 613 TyrValAsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPheCys 632
Db 1141 TATGTCAATTTATTTCTGGGATAAAAAAGAACAAATACTCTCACTTGCACAGATTCTGC 1200
Qy 633 CysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThr 552
Db 1201 TGCCTCATGACCAAAATTCGCAAGGAGTGGAGGGTCTTGGCCTTGAGACTTTTCAACG 1260
Qy 653 AlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSer 672
Db 1261 GCCGAACGGTGCAGTGGCATGGTCATCAGCTGGGAGGCTGATTTGGTCTGAGATAGC 1320
Qy 673 ArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsn 692
Db 1321 CGATTCTGCTCTTTTCCATGAAGATGAAAGACAGCGGAGATCTATGTGGCTTCAAC 1380
Qy 693 ThrSerHisLeuProAlaValGluLeuProGluArgAlaGlyArgTrpGluPro 712
Db 1381 ACCAGCCACTTACCGGCGTGTGTGAGCTCCAGAGCGCGCGGCGGTGGGACCG 1440
Qy 713 ValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspLeuProAspArg 732
Db 1441 GTGGTGGACACAGCAAGCCAGCACCATATGACTTCTCCTCACCAGCACTTACCTGATCGC 1500
Qy 733 AlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSer 752

Db 1501 GCTCTCACCATACACCACTTCTCTCAATTTCTCACTCACTCACTTACCCCATGCTCAGC 1560
Qy 753 TyrSerSerValIleLeuValLeuArgProAspVal 764
Db 1561 TACTCATCGGTCACTCTAGTATTGGCCCTGATGTT 1596
RESULT 8
ABZ12413
ID ABZ12413 standard; DNA; 2352 Bp.
XX AC ABZ12413;
XX XX 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 218.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2000; 2000US-0227866P.
XX PR 26-JAN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX PA (SCEI) SCRIIPS RES INST.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 218; 577pp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b) the
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX SQ Sequence 2352 Bp; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.07e-266 Length: 2352
Score: 2895.50 Matches: 518
Percent Similarity: 81.08% Conservative: 82
Best Local Similarity: 70.00% Mismatches: 127
Query Match: 68.74% Indels: 14
DB: 6 Gaps: 4
US-09-674-817B-3 (1-764) x ABZ12413 (1-2352)

Qy 29 GluAlaAlaThrLysValGluAspGluGlyGluAspGluProValAlaGluAspArg 48
Db 140 GAAGAAGCACCAAGCT-GAAATATCGCGTAGTAGAGAACTCTTAATCAGATAGA 198
Qy 49 TyrAlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68

Db 199 TTTTATCTCCGAT-----GGACTTCCTCTCCATTCGGACCCACC 240
Qy 69 AlaleuAlaGlyValAsnPheAlaValTyrSerGlyValAlaThrAlaAlaLeu 88
Db 241 GTACAGACACGGCGTCATTTCTCTGTTTCTCTACAACTCCGTTCCGTCACATC 300
Qy 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108
Db 301 TGCTTGATTTCTCTCTCCGATCTCCGTCAGAACAAAGTCACGAGGAGATTCAGCTTGAT 360
Qy 109 ProLeuMetAsnArgThrGlyAsnValTyrHisValPheIleGluGlyLeuHisAsn 128
Db 361 CCATCAAGAAATAGAACTGGCCATTTGGCATGTGTTCTGAGAGAGATTTCAAGAT 420
Qy 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
Db 421 ATGTGTGATGTTATAGATTGTATGGCAAGTTTCTCTGAAGAAGTCAATTATTATGAT 480
Qy 149 ValSerAsnValValAlaAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGly 168
Db 481 TCCTCCAAACATTTATTGGATCCTTACGCAAGGCAATTATAAGCAGAGATGAGTTGGA 540
Qy 169 ValProAlaArgGlyAsnAsnCysTyrProGluMetAlaGlyMetIleProLeuProTyr 188
Db 541 GTTTTGGGACCTGATGATAATTGTGGCCTCAATGGCGTATGCTACCCACTCGTAG 600
Qy 189 SerThrPheAspThrGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
Db 601 GAAGAGTTTGAATGGGAAGGGATATGCATCTGAAGCTCCACAGAAAGATCTTGTATA 660
Qy 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
Db 661 TATGAATGCGATGCGGAGTTTTTACAGGCGATGAGTCTAGTAAATGTAATTCCTGGC 720
Qy 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248
Db 721 ACATACCAGGCTGTTGCAGAGAGCTTGACCAATTTGAAGGAGCTTGGATAAATGTATA 780
Qy 249 GluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer----- 266
Db 781 GAATTAATGCCATGTCAGAGTTTAATGAGCTGGAGTATTACAGCTACATACGATTTTG 840
Qy 267 -----LysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 841 GGAGACCACAGGGTAAATTTTGGGTTACTCTACCACTGGGTTCTTCGCGCCATGATC 900
Qy 284 ArgTyrThrSerGlyGlyLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
Db 901 AGATACGCATCAGCAAGCTCTAACAAATTTTGGCTGGACGCCATAAATGAATTCAAAAT 960
Qy 304 PheValArgGluAlaHisLysArgGlyLeuValIleLeuAspValValPheAsnHis 323
Db 961 CTGTGTTAAGAGGACATAAACAGGAGNATTGAGGTAATCATGATGCTCTTGAACAC 1020
Qy 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343
Db 1021 ACAGCCGAAGGAATGAAAAAGGCGCCATTTCTCATTTAGAGAGTTGATAACAGTGC 1080
Qy 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
Db 1081 TATTACATGCTGTCTCAAAAGGGGAGTTCTTAATTAATTATTACGCGTGTGTAATACATC 1140
Qy 364 AsnCysAsnHisProValArgGlnPheIleValAspCysLeuArgTyrTyrPheValThr 383
Db 1141 AACTGCAATCATCTGTGTCGTCATTCATATTGGATTGGCTCGATATTGGGTACA 1200
Qy 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
Db 1201 GAAATGATGTTGTCAGCGCTTTCGCTTTGATCTTGGTTCAATCATGTCAAGGACGACG 1260
Qy 404 LeuTrpAspProValAsnValTyrGlyValaProIleGluGlyAspMetIleThrThrGly 423
Db 1261 CTTTGGGATGCAGCAATGTTTACGGGCTGATGTAGAGGTGACTTGTCTCAACACUGGT 1320

Qy 424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGly 443
Db 1321 ACTCTATTAGCTGCCCTCCAGTAATTGACATGATAAGTAATGATCCAACTACTCGCGGT 1380
Qy 444 ValLysLeuIleAlaGluAlaTyrAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463
Db 1381 GTTAAGCTTAATAGCTGAAGCATGGGATCGGGTGGCTGTACCAAGTTGGCATGTTTCCA 1440
Qy 464 HisTrpAsnValTyrSerGluTyrAsnGlyLysTyrArgAspIleValArgGlnPheIle 483
Db 1441 CACTGGGATATTGCTGAGTGGATGGAATGGAAGTTTCGGGATGTTGTGAGACAGTTCATA 1500
Qy 484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503
Db 1501 AAAGCACCGATGGCTTTTCTGCTGCTTTCTGCTGAATGCTCTGTGGAAGCCCAATCTG 1560
Qy 504 TyrGlnAlaGlyGlyArgLysProTyrHisSerIleAsnPheValCysAlaHisAspGly 523
Db 1561 TACCAG----GGAGGTAGGAAACCTTGGCAGCAGCATCAATTTATATGTGCGCATGATGCT 1617
Qy 524 PheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543
Db 1618 TTTACGTTGGCAGATTTAGTAACCTTACAACTAAGAAATAACTTGGCAATGGGAGAGAG 1677
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAla 563
Db 1678 AATAATGATGAGAGAGATCAAACTTACAGCTGGAACTGTGGAGAGAGGAGACTTTCCG 1737
Qy 564 ArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583
Db 1738 AGTATCTCGTCAAGAGACTAAGGAAACGACAGATCGGAATTTCTTTGTTCCCTCATG 1797
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603
Db 1798 GTTTCCTCCAGGTGCTCCCAATGATTTACATGGAGATGAATATGGCCATCTAAAGGGGA 1857
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGlu 623
Db 1858 AACAAACAACGATATTGCCATGACAACTATATGAACTATTTTCGGTGGGATAAAGGAA 1917
Qy 624 Gln---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642
Db 1918 GAAGCACATCTGACTTCTCAGATTTCTGCGGTATTTCTTATCAAGTTTTCGTGATGAATG 1977
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662
Db 1978 GAATCACTTGGCTTGAATGATTTCCCAACAGCAAGCGTCTGCAGTGGCATGCTTGTCT 2037
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
Db 2038 CCTGAGATCCCAAAATTTGGTCTGAAACAAGTCGATTTGTTGCAATTTTCACTGCTCATCT 2097
Qy 683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
Db 2098 GTGAAGAAAGAAATCTATGTGCGCTTCAACACCAAGTCATTTAGCCACACTTGTTTTCGCTA 2157
Qy 703 ProGluArgAlaGlyArgTyrProValValAspThrGlyLysProAlaProTyr 722
Db 2158 CCGAATAGCCAGGATACCGATGGAGCCATTTGTAGACAGCAAGCAACCGAGCCCTTAC 2217
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742
Db 2218 GACTGCATAACACCGGATCTCCAGAGAGAGAAACGGCGATGAACAGTATAGGCACATC 2277
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762
Db 2278 TTAGATGCAATGATGTACCAATGCTCAGTTACTCATCATCTCTCTCTTCTTTCACCA 2337

RESULT 9
ADA67900
ID ADA67900 standard; DNA; 2352 BP.
XX

AC ADA67900;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Arabidopsis thaliana gene, SEQ ID 141.
 XX
 XX Plant; bacterial infection; fungal infection; viral infection; ds.
 XX Arabidopsis thaliana.
 XX
 XX Arabidopsis thaliana.
 XX
 XX WO2003000598-A1.
 XX
 XX 03-JAN-2003.
 XX
 XX 22-JUN-2001; 2001WO-IB001105.
 XX
 XX 22-JUN-2001; 2001WO-IB001105.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 XX
 XX Identifying at least one gene involved in plant resistance or response to
 XX pathogenic infection for conferring resistance or tolerance to a plant to
 XX bacterial, fungal or viral infection by determining or detecting plant
 XX gene expression.
 XX
 XX Claim 6; SEQ ID NO 141; 899bp; English.
 XX
 XX The present invention relates to a method (M1) for identifying genes
 XX involved in plant resistance or response to pathogenic infection. M1
 XX comprises identifying a gene whose expression is significantly altered in
 XX the incompatible interaction of plant gene expression relative to
 XX expression of the gene in an uninfected plant, in a mutant plant that
 XX does not express a gene associated with response to pathogenic infection,
 XX or in a corresponding incompatible or compatible interaction. (M1) is
 XX useful for conferring resistance to resistance or tolerance to a plant to
 XX bacterial, fungal or viral infection. The present sequence was used to
 XX illustrate the invention.
 XX
 XX SQ Sequence 2352 BP; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 3.07e-266 Length: 2352
 XX Score: 2895.50 Matches: 518
 XX Percent Similarity: 81.08% Conservative: 82
 XX Best Local Similarity: 70.00% Mismatches: 127
 XX Query Match: 68.74% Indels: 14
 XX DB: 7 Gaps: 4
 XX
 XX US-09-674-817b-3 (1-764) x ADA67900 (1-2352)
 XX
 XX QY 29 GluAlaThrLysValGluAspGluGlyGluAspGluProValAlaGluAspArg 48
 XX |||||
 XX DB 140 GAAGAAGCAACGAAGCT-GAAATATCGCGGTAGAGAAACCTCTTAATCAGATAGA 198
 XX |||||
 XX QY 49 TyrAlaLeuGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 58
 XX |||||
 XX DB 199 TTTTATCTCCGAT-----GGACTTCCTTCTCCATTCGAGCCACC 240
 XX |||||
 XX QY 69 AlaLeuAlaGlyValAsnPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeu 88
 XX |||||
 XX DB 241 GTCAGAGACGACGGGTCAATTTCTGTTTACTCTACAACTCCGTTCCGCTACCATC 300
 XX |||||
 XX QY 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluValProLeuAsp 108
 XX |||||
 XX DB 301 TGGTTGATTTCTCTCCGATCTCCGTGACAAACAAAGTACCGAGAGAGATTGAGTTGAT 360
 XX |||||
 XX QY 109 ProLeuMetAsnArgThrGlyAsnValTyrPheHisValPheIleGluLeuHisAsn 128
 XX |||||

DB 361 CCATCAAGGAATAGAACTGGCCATGTTTGGCATGTGTTCTTGAGAGAGATTTCAAGAT 420
 QY
 DB 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
 DB 421 ATGTTGATGTTATAGATTGATGGCAAGTTTCTCTCTGAGAGAGGTCAATATATGAT 480
 QY
 DB 149 ValSerAsnValValAspProTyrAlaLysAlaValLleSerArgGlyGluTyrGly 168
 DB 481 TCCTCCAACTTTATTGGATCTTACGCAAGCAATTATTAAGCAGAGATGAGTTTGA 540
 QY
 DB 169 ValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyr 188
 DB 541 GTTTTGGACCTGATGATAATTGTGGCTCAAAATGGCGTGTATGGTACCCACTCGTAG 600
 QY
 DB 189 SerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
 DB 601 GAAGAGTTTGTATCGGAAGGGGATATGATCTGAAGCTTCCACAGAAAGATCTTGTATA 660
 QY
 DB 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
 DB 661 TATGAAATGCAATGTCGAGGTTTACAAAGGCATGAGTCTAGTAAATTTGAATTCCTGGC 720
 QY
 DB 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248
 DB 721 ACATACCAGGGTGTGCAGAGAACCTTGACCAATTTGAAGGAGCTTGGATAAATTTGATA 780
 QY
 DB 249 GluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSer----- 266
 DB 781 GAATTAATGCCATGTCACGATTTAATGAGCTGAGTATTACAGTCAACAATGCAATTTG 840
 QY
 DB 267 -----LysMetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThr 283
 DB 841 GGAGACACACGGGTAAATTTTGGGTTACTCTACCATTTGGTTCCTCTCGCCCATGATC 900
 QY
 DB 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
 DB 901 AGATACGCATCAGCAAGCTCTAACAAATTTGCTGCAGCAGCCATAAATGAATCAAAAT 960
 QY
 DB 304 PheValArgGluAlaHisLysArgGlyIleGluValLleLeuAspValValPheAsnHis 323
 DB 961 CTGTGTTAAGAGGACATAAACAGGAAATTGAGTAATCATGATGTCGTCTGAACAC 1020
 QY
 DB 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsnThrThr 343
 DB 1021 ACAGCCGAAGGGAATGAAAAAGGGCCCATTTCTCATTTAGAGAGTTGATAACAGTGC 1080
 QY
 DB 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
 DB 1081 TATTACATGCTTGTCTCCAAAGGGCGAGTTCTATAATTTATTCAGGCTGTGTATAATC 1140
 QY
 DB 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTyrValThr 383
 DB 1141 AACTGCATCATCTGTGGTGGCTCATTTATTTGATTTGCCTGAGATTTGGTTACA 1200
 QY
 DB 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
 DB 1201 GAAATGATGTTGACGGCTTCCGCTTTGATCTTGGTTCAATCATGTCTCAAGAGCAGCAGC 1260
 QY
 DB 404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423
 DB 1261 CTTTGGGATGACGCAATGTTTACGGGCTGTAGTAGAGTCACTGTCTCAACATGGT 1320
 QY
 DB 424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGly 443
 DB 1321 ACTCCTATTAGTCCCTCCAGTAATTCATGATAGTAATGATCCATACATCTCCGCGT 1380
 QY
 DB 444 ValLysLeuIleAlaGluAlaThrAspAlaGlyGlyLeuTyrGlnValGlyGlnPhePro 463
 DB 1381 GTTAAGCTAATAGCTGAAGCATGGATGCGGGTGGCTGTACCAGTTGGCATGTTTCCA 1440
 QY
 DB 464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483
 DB 1441 CACTGGGGTATTGGTCTGAGTGAATGGAAGTTTCGGGATGTTGTGAGACAGATTCATA 1500

QY 301 PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320
 DB 419 TTTAAGTATCTTGTCAAGGAGACACATAAAGCTGGATCGAGTTATCATGGATGTGTT 478
 QY 321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp 340
 DB 479 TTCAATCACACTGCTGAAGAAATGAAATGGTCCCATACTATCATTTAGAGCATTTGAC 538
 QY 341 AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360
 DB 539 AACAGTGTGTTTATACGCTAGCTCCCTAAGGGTGAATTTTACAACTACTCAGATGTGA 598
 QY 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
 DB 599 AATACCTTCAACTGTAATAATCCCATTTGATGATGATGATGATGATGATGATGATGAT 658
 QY 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
 DB 659 TGGTTTACCGAAATGCCAGTAGATGGCTTCGGTTTGTATCTTCTATCTTCAAGA 718
 QY 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
 DB 719 AGTAGAGCTCGTGAATGCTGTAATGCTATGGAATTCATTCAGCTGACATGATC 778
 QY 421 ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle 440
 DB 779 ACCACAGGCATCTCTCACAAAGCCCACTTGAATGATGATGATGATGATGATGATGATGAT 838
 QY 441 LeuGlyGlyValLysLeuIleAlaGluAlaTyrAspAlaGlyGlyLeuTyrGlnValGly 460
 DB 839 CTATAGTGAGTAAAGCTTATAGCTGAAGCATGGATTTGTGGAGCCCTTACCAAGTTGGC 898
 QY 461 GlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArg 480
 DB 899 ATGTTTCCGCACTGGGTATCTGCTGGAGTGAACCGAAAGTACCGTGACATGGTACGT 958
 QY 481 GlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuGlySer 500
 DB 959 CAGTTTCATCAAGGACATGATGGTCTTCTGGGGCTTTTCTGAAATGCCCTTTGTGAAGC 1018
 QY 501 ProHisLeuTyrGlnAlaGlyGlyValArgLysProTrpHisSerIleAsnPheValCysAla 520
 DB 1019 CCAATCTATACAGAGAGGAGGAGAAACCACTGGAACAGTATAAATTCGTGTGTGCC 1078
 QY 521 HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn 540
 DB 1079 CACGATGGTTTACTTTGGCTGATTTTATGACATACAAACAATTAACACAAATTTGGCAAT 1138
 QY 541 GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGly 560
 DB 1139 GGAGAGGACAAAGATGGGAGAAATCACATAATAGTTGGATTTGGCGAGGAGGA 1198
 QY 561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580
 DB 1199 GAATTTGCAATATCTTTGTGAAGAAATGAGGAAAGACAAATTCGGAACTTCTTCCTC 1258
 QY 581 CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr 600
 DB 1259 TGCCTTATGGTTTCCCAAGGTGTTTCCCATGATATATATGGTGTATGATATGATGATGAT 1318
 QY 601 LysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAsp 620
 DB 1319 AAGGAGGAAACAACAACATGATTCGATGACAAATATATTAATTAATTAATTAATTAATTAAT 1378
 QY 621 LysLys---GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArg 639
 DB 1379 AAGAGAGATGAATCTTCATCTGATTTTGTGAGATTTTTCGGCTCATGACAAATTCGCG 1438
 QY 640 LysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHis 659
 DB 1439 CATGAATGTGAATCACTGGGATTAGATGGTTTCCCTACAGCAGAAAGGCTGCAATGGCAT 1498

QY 660 GlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMet 679
 DB 1499 GGTCACTCTCCAGAACTCCAGATTCGATGAAACAAAGTCGATTCGTTGCATTTACACTG 1558
 QY 680 LysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaVal 699
 DB 1559 GTCACAAAGTGAAGGAGAACTATATATTCCTTTAAGCCAGCCCAATTTGCCCTGTAAAG 1618
 QY 700 ValGluLeuProGluArgAlaGlyArgTrpGluProValValAspThrGlyLysPro 719
 DB 1619 ATTACACTTCCAGAAAGCCTGTTATAGATGGCAGCCGTTTGGACACAGGCAACCA 1678
 QY 720 AlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739
 DB 1679 GCACCAATTCCTTCCAGACAGCATGTTCTCCTGAGAGAGACAGCAGCAGCAACAATAT 1738
 QY 740 SerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuVal 759
 DB 1739 TCTCATTTCTGGAGCGCAACCACTATCCGATGCTCAGTTATTCATCATTCATTCCTTTA 1798
 QY 760 Leu 760
 DB 1799 CTA 1801
 RESULT 11
 AAX34655
 ID AAX34655 standard; DNA; 9289 BP.
 AC AAX34655;
 DT 17-OCT-2003 (revised)
 DT 05-JUL-1999 (first entry)
 DE Hexaploid wheat DBE genomic sequence.
 KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
 KW grain softness protein I; bacterial isomylase; glycogen synthase;
 KW WSBE I-D4 gene; ss.
 OS Aegilops tauschii.
 FH Key Location/Qualifiers
 CDS 1..9287
 FT /*tag= a
 FT /note= "the start codon is not indicated; contains 146
 internal stop codons"
 XX WO9914314-A1.
 PD 25-MAR-1999.
 PF 11-SEP-1998; 98WO-AU000743.
 XX 12-SEP-1997; 97AU-00009108.
 PR 20-MAR-1998; 98AU-00002509.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (AUSU) UNIV AUSTRALIAN NAT.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LINA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 PI Li Z, Morell M, Rahman S;
 XX WPI: 1999-229525/19.
 DR P-PSDB; AAY06919.
 XX New isolated cereal plant enzyme genes used for, e.g. expression of
 PT antisense sequences of granule bound synthase.
 PS Claim 14; Page 103-115; 171pp; English.

CC The invention relates to a novel enzyme of starch biosynthetic pathway in
 CC a cereal plant, where the enzyme is selected from starch branching enzyme
 CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
 CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
 CC rice or maize. The methods and products can be used for targeting
 CC expression specifically to the endosperm of the seeds of cereal plants
 CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.
 CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the wheat DBE genomic DNA sequence. (Updated
 CC on 17-OCT-2003 to standardise OS field)

XX Sequence 9289 BP; 2477 A; 1909 C; 2040 G; 2863 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.71e-214 Length: 9289
 Score: 2359.50 Matches: 655
 Percent Similarity: 27.25% Conservative: 7
 Best Local Similarity: 26.97% Mismatches: 16
 Query Match: 56.02% Indels: 1757
 DB: 2 Gaps: 18

US-09-674-817b-3 (1-764) x AAX34655 (1-9289)

Qy 2 GlyProAlaProArgLeuArgArgTyrArgProAsnAlaThrAlaGlyLysGlyValGly 21
 Db 1948 GGGCGGCGCGCGCGCTCGACGCTGGCGACCCCAATCGCGCGGCGGAGGGGTCGGC 2007
 Qy 22 GluValCysAlaAlaValAlaGluAlaAlaThrLysValGluAspGlu---GlyGluGlu 40
 Db 2008 GAGGTGTGCGCGCGGTGTTCGAGCGCGCGACGAAGCCGAGGATGAGGACGACGAG 2067
 Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyCysArgValLeuAlaGly 60
 Db 2068 GAGGAGCGGTGGCGGAGGACAGTACGCTCGCGCGCGCGTGCAGGGTGTCTGCGCGGA 2127
 Qy 61 MetProAlaProLeuGlyValAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80
 Db 2128 ATGCCCGCGCGCTGGGCGCACCGCTCGCGCGGGGTCAATTTTCGCGCTCTACTCC 2187
 Qy 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97
 Db 2188 GGTGGAGCCACCGCGCGCGCTCTGCTCTTTCACGCGCAGAGATCTCAAGGGCGGTGGG 2247
 Qy 97 ----- 97
 Db 2248 TTGCTCCCGGTAGAGTTTCATCAGCTTTCGTCGCGCGCGCGCCCTTTTCGGCTG 2307
 Qy 98 -----Ala-AspArgValThrGluGluValProLe 107
 Db 2308 CGATTTAAGTTTTCCTACTGGGGGAATGCTGCAGGATAGGTGCACGGAGAGGTTCCCT 2367
 Qy 107 uAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGluLeuHi 127
 Db 2368 TGACCCCTGTGAATCGAGTGGGAACGTGTGGCATGTCTTATTGAAGCGGAGGTGCA 2427
 Qy 127 sAsnMetLeuThrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe 147
 Db 2428 CGACATGCTTTACGGGTACAGTTTCGACGCGCACCTTTGCTCCCTCAGTCCGGGCATCCT 2487
 Qy 147 uAspValSerAsnValValAspProTyrAlaLys----- 159
 Db 2488 TGATATTTCCAATGTCGTGGTGGATCCTTATGCTTAAGGTGATCATACTTTAGCTTTACCT 2547
 Qy 159 ----- 159
 Db 2548 GCATCTGGTATTTACAGTAAATTTGTTAGTGGACCCCTATTGTTGGCTTTTGTT 2607
 Qy 160 -----AlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTr 177
 Db 2608 GCTCTAGGAGTGTATAGCCGAGGGAGTATGGGTTCCGGCGCGTGGTAACAAATTGCTG 2667

Qy 177 pProGlnMetAlaGlyMetIleProLeuProTyrSerThr----- 190
 Db 2668 GCCTCAGATGGTGGCATGATCCCTCTTCATATAGCAC-GGTATGCCCTGATTGCTGAAA 2726
 Qy 190 ----- 190
 Db 2727 ATATTGGCTGCAATTGTTCTCTCTTTTCTCATATTTTCTCCTGCTCTTCCTGTTGAC 2786
 Qy 190 ----- 190
 Db 2787 TACATTGCCCTCAGACAGTCATGATCAAAGAGAGCAGTGTGTCATTAGACATTTTGTAGTTGTC 2846
 Qy 190 ----- 190
 Db 2847 TGCTGACTTTGACCACAAACTTGTAAATTTACTGTTGTTAAAGTCTCTGAATCATATTTT 2906
 Qy 190 ----- 190
 Db 2907 TTATAATATTATGTTTGGCAAGTGAAGTAAAGTGAATGTCATCTAGTATTTGTTGTTCC 2966
 Qy 191 -----PheAspTyrG 194
 Db 2967 TGTCTTAGTGTGTTAATTGGACATGCAGTAAAGGTTTGGCATCTGCAGTTTGTATGGGA 3026
 Qy 194 uGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuAr 214
 Db 3027 AGCGACCTACCTCTTAAGATATCTCAAAAGAGCCTGGTAATATATGATGATGTCATTTGGC 3086
 Qy 214 gGlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVa 234
 Db 3087 TGGATTACGAAGCAGTATTCAGCAATGTAGAACATCCGGGTACTTTTCATTGGAGCTGT 3146
 Qy 234 lSerLysLeuAspTyrLeuLys----- 241
 Db 3147 GTCGAGGCTTGACTATTTGAAGGTACAGCTGTCTGTGCTACTACATAGGATAAATTTTA 3206
 Qy 241 ----- 241
 Db 3207 AAGAAAGCTACATATTAGCCAGAATTTGGTTTATTACAAAACACTACTGCATACTAGCA 3266
 Qy 241 ----- 241
 Db 3267 GTTACATGCTCATTTATTCGAGGAGATGCTCACAGCATCTTATTTGGATTTTATACCCAAT 3326
 Qy 242 -----GluLeuGlyValAsnCysIleGluLeuM 251
 Db 3327 TCTGTTTTCATATTGGACTGTTCCTCTACAGGAGCTTGGAGTTAATTGTTATGAATTAA 3386
 Qy 251 etProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer----- 265
 Db 3387 TGCCCTGCGCATGATGATCAACGAGCTGGAGTACTCAACCTCTTCTTCCAAAGTAAGGACATG 3446
 Qy 265 ----- 265
 Db 3447 AATTAGTATTAGCTGCCAGCATGTTGTTGAGTGAAGTTCATACACATTTTGTGCGCTGC 3506
 Qy 265 ----- 265
 Db 3507 ATAACGTATATTGTTCAAACTATT-----TTTAGCAGTCACTCAACAGTTTTTACATATA 3566
 Qy 265 ----- 265
 Db 3567 TATAATATAGACTATTTCGTCACCCCTGGGTGAGGAATAGTTATTCACCCACCTCTATT 3626
 Qy 265 ----- 265
 Db 3627 TTAAACATCTATGCACCGTAATTTTACGTTTCGTAATTTGCTTATTTTAGAGATAAAAA 3686
 Qy 265 ----- 265
 Db 3687 GAGAACGTAAGAAAAACCTATATATCGTTCGTAATAAAAAAATATGTTACGTAAAAATACAAAT 3746

[illegible]

D5	4825	TATACATTTTACTTCTAGAACTACTTTTTCATTTCTTTTCTGCTGCTGTCATTTTGATATG	4884
QY	377	-----	377
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QY	377	-----	377
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QY	378	-----	382
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D5	5065	GATGGAATGCATGTTGATGGTTTCGTTTGATCTTCGATCCATAATGACCAGAGGTTTC	5124
QY	402	I-----	402
D5	5125	CAGGTAATTTGCTATTATTGTTTGTGCTGTGTCCTTTTTCAGAAGATCTTTAAAGAA	5184
QY	403	-----	418
D5	5185	TGTTCTTTTACAAAGCTCTGGGATCCAGTTACGTTATGAGCTCCCAATAGAAGGTGA	5244
QY	418	pMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAs	438
D5	5245	CATGATCACAAACAGGGACACCTCTTGTTACTCCACCACCTTATTGACATGATCAGCAATGA	5304
QY	438	pProIleLeuGlyGlyVallys-----	445
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QY	445	-----	445
D5	5485	ACTGTATATACTTGACATATATTGCTTCCTGGAGGCTCTCTATTCTCTTCCCCCGT	5544
QY	446	-----	462
D5	5545	TGCAATTTATAGCTCATTTGCTGAAGCATGGATGATCAGGAGCCCTCTATCAAGTAGGTCAAT	5604
QY	462	heProHisTrpAsnValTrpSerGluTrpAsnGlyLys-----	474
D5	5605	TCCCTCTACTGGAAATTTGGTCTGAGTGGAAATGGGAA-GGTAAGGTACCTGTTTAAAGATT	5663
QY	474	-----	474
D5	5664	TGAATGGCAAAATACTGTAGAAAATATAAATTTATATTGTCACATATATAGATAAAGCAA	5723
QY	474	-----	474
D5	5724	ATAATACGCATTCACCTGAACTTTAAGGGGCACGCAGAAATTTATCCCGCATCTGTCTAC	5783
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D5	5784	AAGAAATGATAACACATGTGCTGAATAGTGAAGTACTACTTCTCAAATGTTCTGAATGAACG	5843
QY	474	-----	474
D5	5844	CACTAACCTCTTTGAGTGTCAACCGAGCAGAGAAATATTTCAGTTTTTCTGCAAGAAATGTT	5903
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QY 614 ----- 619
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QY 641 ----- 655
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AC AAD42891;
XX
DT 24-FEB-2003 (first entry)
XX
DE Maize sugary1 (SUI) gene.
XX
KW Maize; starch debranching enzyme; sugary1; industrial application; SUI;
XX starch processing industry; ds.
XX
OS Zea mays.
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Db 2684 ACAGTTTCGATGGCGTGTTCGCCCTTGAGCGCGACAGTACTACGATGTGTCCACGTTG 2743
Qy 153 alValAspProTyrAlaLys----- 159
Db 2744 TGGTGGATCCATACGCTAAGGTGACGGCTGTTGTCTTTACTTTGGCTATGCGTGTGAGC 2803
Qy 159 ----- 159
Db 2804 TGTGACACACTCAGAAACTGATGCTGGGTGCTGTGCTCATGTTTATGTTGTTTACTTCTT 2863
Qy 160 -----AlaValIleSerArgGlyGluTyrGlyValProAla 171
Db 2864 CTTGTTGTTGTTTCTCTAGCGAGCAGTGTGAAGCGAGGTGAATATGTTGTGCTGCG 2923
Qy 172 ArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSer----- 189
Db 2924 CCTGGTGTAGTTGTTGGCTCAAAATGGCTGGTATGATGATCCCTCTCTCCCTATAAAGTA 2983
Qy 189 ----- 189
Db 2984 AGCCAGAACTACTCTCGCTCACACTACTCTTCCTGTTGTTGCTTTCATGCTGTATCCTTCTCT 3043
Qy 189 ----- 189
Db 3044 TCCAGTTTATGATCTCCCATGCTGACTCACTCACTGATTAACAATAAAGAAACCA 3103
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Db 3104 CCGCATATATTGGCTCATTTGATGATTTGAAAGCTCCCGCATGAACTAACTGAACAAG 3163
Qy 189 ----- 189
Db 3164 CGCTAGATATCAACTGTAGTTAGGACTCATTTGGCTTCCTGTTACTTAGTTTCTGCTTT 3223
Qy 189 ----- 189
Db 3224 GCCAGTTCAAAATGGAGTCCGAAGTTATATTTCAGTCTATTCATGTTGTCTTTGTTATT 3283
Qy 190 -----Thr-PheAspTrpGluGlyAspLeuProLeuAr 200
Db 3284 CATTTGATGATAGAGTTTTCGATTTGCAATTTGATTTGCAAGGTGACCTTACCTTGG 3343
Qy 200 gTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAs 220
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Qy 240 uLys----- 241
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Qy 241 ----- 241
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Qy 241 ----- 241
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Qy 242 -----GluLeuGlyValAsnCysI 248
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Qy 267 ----- 267
Db 4184 TCACAACTGACTTATATTCATATATTCACACATTAATTTTCATATAATTTGTTTCATCTTGTG 4243
Qy 268 -----MetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThrArgTyrT 286
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Db 4544 TTTAGGGGATAGATAAATAGTACATCTACTGCTTGCACCTAAGGTGAGATACATTATT 4603
Qy 350 ----- 350
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Qy 351 -----GlyGluPheTyrAsnTyr 356
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Db 4724 TTCGTTTGTGGAATACCTTCAATTTGTAATCATCTCTGTAGTCCGTGATTTTATAGTGA 4783
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 Db 7904 ATCGCGATACCGTGGTTCAGTTCATCAAAAGGACACAGATGGATTTGCTGGTCTTTGCTG 7963
 Qy 495 luCysLeuCySGlySerProHisLeu----- 503
 Db 7964 AATGCTATGTGGAAGTCCACA-GTTATACCAGTAAATGTAGCATAGTACCCATCAATG 8022
 Qy 503 ----- 503
 Db 8023 AGCAGGTGCTACATGACCTGAACAGAAACTTTTGAAGAACTGGGTGATAGTGTACAG 8082
 Qy 503 ----- 503
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Qy 503 ----- 503
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 Qy 503 ----- 503
 Db 8203 TCTTTTCTTGAGTGTCTAATGAGACCTCTTCAAGCCATTTGAAACTCTCTACTATATATGT 8262
 Qy 503 ----- 503
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 Qy 503 ----- 503
 Db 8323 TAACAATGAATGCGAATACTCTCCATGTATTGTATGTAATTAGGTGGATTAGTGTATC 8382
 Qy 504 -----TyrGlnAlaGlyGlyArgL 510
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 Qy 510 ysProTriPheIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuV 530
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 Qy 530 alThrTyAsnLysLysTyAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnH 550
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 Qy 550 isAsnLeuSerTrpAsnCysGlyGlu----- 558
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 Qy 558 ----- 558
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 Qy 558 ----- 558
 Db 8683 CCAAACTGTTTCACTAAACAGGCTATATAGTTTGTACAGTGCATTTCCAGCTAAAT 8742
 Qy 558 ----- 558
 Db 8743 TATGTGGCAAGTATATACAGATCATCTCTATAGTGTAGGCACCTTTAGAGTTTCATTGA 8802
 Qy 559 -----GluGlyGlyPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMet 575
 Db 8803 ATAATCGCAAGAGAGAAATTTGCAAGTCTGTCAAGTCCGAAGATTAAAGGAAGGCAATG 8862
 Qy 576 AsAsnPhePheValCysLeuMetValSerGln----- 586
 Db 8863 CGCAATTTCTTTGTTGTTCTTATGTTTCTCAGGTAAGNAATTAGTATCTGATGTTTTTAAG 8922
 Qy 586 ----- 586
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 Qy 586 ----- 586
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QY 586 ----- 586
Db 9223 AGGGTAAGTTAAAGTGGATCTCGAAGTCACATTGTTATTTTTTGTATGATCTACTACT 9282
QY 587 ----- GlyValProMetPheTyrMetGlyAs 595
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QY 595 pGluTyrClyHisThrIysGlyGlyAsnAsnThrTyrCysHisAspSerTyrVal-- 614
Db 9343 TGAATATGTCACACAAAGGGAGGAAACAACATACGTACTGTCATGCGCATGACCATATGT-CA 9401
QY 614 ----- 614
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QY 615 ----- AsnTyrPheArgTyrAspIysLys---G1 623
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QY 623 uGlnTyr-SerGluLeuHisArgPheCysCysLeuMetThrIysPheArgLys----- 640
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QY 641 -----G 641
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QY 679 ----- 679
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QY 721 roTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerH 741
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QY 741 isPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuA 761
Db 10122 ATTTCCTCAACTCCAATCTCTATCCTATGCTACGTACTCTCTCTCATCATCTCTTGTATTCG 10181
QY 761 rgProAspVal 764
Db 10182 GCCCTGATGC 10192
RESULT 13
AAD47817
ID AAD47817 standard; DNA; 10439 BP.
XX
AC AAD47817;
```

```
XX
DT 24-FEB-2003 (first entry)
XX
DE Alternative version of maize sugary1 (SU1) gene.
XX
KW Maize; starch debranching enzyme; sugary1; industrial application; SU1;
KW starch processing industry; ds.
XX
OS Zea mays.
XX
PN US6410716-B1.
XX
PD 25-JUN-2002.
XX
PF 24-FEB-1999; 99US-00256741.
XX
PR 24-MAR-1995; 95US-00410784.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Myers AM, James MG;
XX
DR WPI; 2002-616514/66.
XX
PT Novel starch debranching enzyme protein sugary1 or its polypeptide
PT fragment useful as replacement for bacterial and fungal enzymes currently
PT used in starch processing industry.
XX
PS Disclosure; Fig 2; 75pp; English.
XX
CC The invention relates to maize starch debranching enzyme, sugary1 (SU1)
CC and nucleic acid molecules encoding such proteins. SU1 sequences are used
CC as a replacement for the bacterial and fungal enzymes currently used in
CC the starch processing industry and as immunogens to raise antibodies
CC against SU1. Polynucleotides of the invention are useful as markers for
CC identification of specific corn varieties, for the development of corn
CC varieties with starch properties tailored for specific industrial
CC applications. The present sequence is an alternative version of maize SU1
CC gene. Note: This sequence is stated to be the same as that shown as SEQ
CC ID NO:3 (AAD42891) in column 41-52 of the specification. However the
CC sequences differ
XX
SQ Sequence 10439 BP; 2847 A; 2237 C; 2187 G; 3168 T; 0 U; 0 Other;
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Alignment Scores:
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Score: 2179.00 Matches: 649
Percent Similarity: 25.80% Conservative: 46
Best Local Similarity: 24.09% Mismatches: 67
Query Match: 51.73% Indels: 1937
DB: Gaps: 21
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QY 21 yGluVal-----CysAlaAlaValValGluAlaAlaThrLysValG1 35
Db 858 GCGGTGTCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGA 917
QY 35 uAspGluGlyGluGluAspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCY 55
Db 918 GGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 977
QY 55 sArgValLeuAlaGlyMetProAlaProLeuGlyValAlaThrAlaLeuAlaGlyValAs 75
Db 978 CCGGTGTCTCGGGAATGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTGCAA 1037
QY 75 nPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAs 95
Db 1038 CTTCCGCGTCTACTCCAGCGGTGCTCGCGCGCGCGTGTGCTGTGCTCTTCGCTCCGCGGA 1097
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Db 3255 TACATTATTCATCTGTGAATCGTTCTTTTCATGGACCAACAAAGTATTATGTATTTCATTT 3314
QY 351 -----GlyluPh 353
Db 3315 CATAGATTCAGCTATATATAACAGCTATTTTGAAGACATTTATTTGTGAGGAGAGATT 3374
QY 353 eTyraSntTy+serGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPh 373
Db 3375 TTATAATTATTTCTGTTGTGGAATACCTTCAATTGTAATCACTCTGTAGTCGCTGAATT 3434
QY 373 eileValaspCysLeu----- 378
Db 3435 TATAGTCGATTTGCTTGGAGTACAAAATCTGTATATAACTTCTGTAAATTCTCTCTAATT 3494
QY 378 ----- 378
Db 3495 CTTTCTGCCGCTGTCTCAATCTATTGGATGATGCAAGTTTTTGGGGATGATAGCAATGT 3554
QY 378 ----- 378
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QY 378 ----- 378
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QY 379 -----ArgTyTrrpValTh 383
Db 3675 TGTTAAGATAAATTTGTTATGCACTAATAATTTGAGTTTGATGTTGCAGATCTGGGTAAAC 3734
QY 383 xGluMetHisValaspGlyPheArgPheAspLeuAlaSerIleMetThrArgGly----- 401
Db 3735 AGAAATGCATGTTGATGGTTTTTCGTTTTCGTTTTCACCTTTCATCTATATACTGACCCAGAGGATGCAG 3794
QY 401 ----- 401
Db 3795 GTAAAAATGTATTCTTATTTCTCCTTATTTTGTCTTTTGTAGGCATTCCTTAAGCCAACT 3854
QY 402 -----SerSerLeuTrpaspProValAsnValTyGlyAlaProIleGluGlyaspMe 419
Db 3855 TTCCTTTACCAGTCTATGGGATCCAGTTAATGTGTATGGAAGTCCCAATGGAAGTGACAT 3914
QY 419 tIleThrThrGlyThrProLeuValThrProProLeuIleaspMetIleSerAsnaspPr 439
Db 3915 GATTACAGACGGGACACTCTTGTTGCCACCACCTTATTGACATGATTAGCAATGACCC 3974
QY 439 oIleLeuGlyGlyVallys----- 445
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QY 445 ----- 445

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QY 445 ----- 445
Db 4455 AGGTTTCATCAACAGCAGGAGTAAGGTGGCCCAAGCTGAAAGGAGATAAAAATACTGAACCA 4514
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QY 445 ----- 445
Db 4575 ACATAAGGAGCAAGCATCTGGATGTGGCAACCTCTCTTTTCAACCTGTACAGCGTCCA 4634
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QY 445 ----- 445
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QY 445 ----- 445
Db 4815 TAATTCAACCCCTCACTGAATCCCATAAACAGCAGGTACTGCTGACGCCAGCCAGCGAG 4874
QY 445 ----- 445
Db 4875 AGAGGTGCTTTAATATCCCTAACCCACTGCCAATTTTCAAGGCTGAGCCACAGTTCTT 4934
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Db 4935 GAATATAGAATCTTTTGGCCACCTTAGCTACCACTCAGGGGCAAAATCCCTGATCGCA 4994
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QY 445 ----- 445
Db 5115 CAAGGCTGTTTGGGTCCATTTTTTTTCCAAACCAATTAACCATTTTGTATGAAAGCCAGCT 5174
QY 445 ----- 445
Db 5175 CATGAATTGCAGATTAGGGAATTTCCCAAGCCCCCAAGATCAATAGGCTTGTAAACAATA 5234
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Db 5235 TCTCAAGAAACCAAGAGCTGCCCTCCATTAGCCTCTTTCTCTTCTTCCAAATAAACCCC 5294
QY 445 ----- 445
Db 5295 CTTCTAATTTTGTCTATAGCTTTAATCATCCAAATTTGGATATTCAATTGCAATAAGAGATA 5354
QY 445 ----- 445
Db 5355 GACTGGGATAGCGAAGGCACATATCGCACAGAGCTATTCTACCGCAAGGTTAAGAAG 5414
QY 445 ----- 445
Db 5415 ATGTGCTTTCCAAATTTGCAATAAGAGGTTATTTGGTGTGATTATGATTCTTTAATACTTAT 5474

Qy 752 SerTyreSerValIleLeu 758
Db 2297 COGTACTGCTATGCTTCTT 2317

Search completed: August 10, 2004, 01:34:49
Job time : 842 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2004, 00:58:30 ; Search time 135 Seconds

(without alignments)
3140.611 Million cell updates/sec

Title: US-09-674-817B-3

Perfect score: 4212

Sequence: 1 SGAPRLRRWPNTAGKV.....SNLYPMLSYSSVILVRPDV 764

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued_Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3569.5	84.7	2700	4	US-09-731-166-15
2	3528.5	83.8	2712	2	US-08-410-784A-1
3	3029	71.9	2706	4	US-09-463-238-2
4	2923	69.4	2806	4	US-09-463-238-11
5	2612	62.0	2133	3	US-09-187-124-1
6	2612	62.0	2133	4	US-09-850-936-1
7	1577	37.4	2634	4	US-09-463-238-3
8	1305.5	31.0	1230025	4	US-09-198-452A-1
9	1225	29.1	4403765	3	US-09-103-840A-2
10	1225	29.1	4411529	3	US-09-103-840A-1
11	1187	28.2	2181	3	US-09-129-075-3
12	1187	28.2	2181	3	US-09-346-237-12

13	1187	28.2	2181	4	US-09-544-123-3	Sequence 3, Appli
14	1122.5	26.7	1944	4	US-09-252-931A-8062	Sequence 8062, Ap
15	1032.5	24.5	1389	4	US-09-463-238-12	Sequence 12, Appl
16	1014	24.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
17	1014	24.1	1830121	4	US-09-543-990A-1	Sequence 1, Appli
18	998.5	23.7	2151	4	US-09-489-039A-3670	Sequence 3670, Ap
19	915.5	21.6	2843	4	US-09-463-238-1	Sequence 1, Appli
20	915.5	21.6	2843	4	US-09-463-238-10	Sequence 10, Appl
21	810	19.2	2334	5	PCT-US95-09323-1	Sequence 1, Appli
22	810	19.2	2334	5	PCT-US95-09323-1	Sequence 1, Appli
23	807	19.2	2244	1	US-08-476-519-10	Sequence 10, Appl
24	807	19.2	2244	5	PCT-US95-09323-10	Sequence 10, Appl
25	804.5	19.1	2625	6	5457037-4	Patent No. 5457037
26	804.5	19.1	3336	6	5457037-1	Patent No. 5457037
27	781	18.5	1671	4	US-09-252-991A-8261	Sequence 8261, Ap
28	779.5	18.5	2253	6	5457037-2	Patent No. 5457037
29	652	15.5	2523	2	US-08-410-784A-3	Sequence 3, Appli
30	544.5	12.9	2781	4	US-09-313-677-1	Sequence 1, Appli
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32	544.5	12.9	2799	4	US-09-313-677-18	Sequence 18, Appl
33	544.5	12.9	7026	4	US-09-313-677-20	Sequence 20, Appl
34	544.5	12.9	7344	4	US-09-313-677-16	Sequence 16, Appl
35	519	12.3	2319	4	US-09-134-078-14	Sequence 14, Appl
36	516	12.3	2766	4	US-09-514-599-1	Sequence 1, Appli
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38	506.5	12.0	2784	1	US-08-477-630-10	Sequence 10, Appl
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41	506.5	12.0	2784	1	US-08-478-341-10	Sequence 10, Appl
42	506.5	12.0	2784	3	US-08-996-733-10	Sequence 10, Appl
43	506.5	12.0	4464	1	US-08-474-140-8	Sequence 8, Appli
44	506.5	12.0	4464	1	US-08-474-140-9	Sequence 9, Appli
45	506.5	12.0	4464	1	US-08-477-630-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-731-166-15
; Sequence 15, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Sul isoamylase -- Genbank Accession No. 6639126 AF030882
; NAME/KEY: CDS
; LOCATION: (88)...(2457)
US-09-731-166-15

Alignment Scores:
Pred. No.: 0
Score: 2569.50
Percent Similarity: 90.28%
Best Local Similarity: 84.59%
Query Match: 84.75%
DB: 4
Length: 2700
Matches: 653
Conservative: 65
Mismatches: 10
Indels: 4
Gaps: 4
US-09-674-817B-3 (1-764) X US-09-731-166-15 (1-2700)

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 QY 394 uAlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPr 414
 Db 1341 TGCACTATACCTGACAGAGGATGAGTCTATGGATCCAGTCAATGTATGTATGAGATCC 1400
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 Db 1401 AATGGAGGTGACATGATACACAGGACACCTCTTGTTCGCCACACCTATATTGACAT 1460
 QY 434 tIleSerAsnAspProIleLeuGlyGlyValIleLeuIleAlaGluAlaTrpAspAlaGl 454
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 Db 1521 AGTCTCTATCAAGAGGTGAGTCTTCTCACTGGAACCTTTGGTCAGATGGAAAGAAA 1580
 QY 474 sTyrArgAspIleValArgGlnPheIleLeuGlyThrAspGlyPheAlaGlyPheAl 494
 Db 1581 GTATCGCATACCGTGGCTCACTTCATCAAGGACACAGATGATTCGTGCTTTGTC 1640
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 QY 514 rIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLy 534
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 QY 534 sIysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTr 554
 Db 1761 CAAGTACAACTTGTCAATGTGGAGACTTCAGAGATGGGAAATCATATCTTAGCTG 1820
 QY 554 pAsnCysGlyGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGl 574
 Db 1821 GAATGTGGGAGGAGGAGGAGATTTGCAAGTCTGTCTGCGAAGATTAAAGGAAGGCA 1880
 QY 574 rMetArgAsnPheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGl 594
 Db 1881 AATGGCAATTTCTTTGTTTGTATGTTTCTCAGGGAGTTCCAAATGTTCTACATGGG 1940
 QY 594 yAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrVa 614
 Db 1941 CGATGAATATGTGTACACAAAGGAGGAGGAAACAACATACGTACTGCCATGACCATATGT 2000
 QY 614 lAsnTyrPheArgTrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCy 633
 Db 2001 CAATATTATTTCCGTTGGGATAGAGAGAGAAACAATCTCTGATTGTACAGATTCTCGCG 2060
 QY 633 sLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAl 653
 Db 2061 TCTCATGACCGAATTCGCAAGAAATGTGAATCTCTTGGCCTTGAGGACTTCGCCACTTC 2120
 QY 653 aLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerAr 673
 Db 2121 AGAAGCGTTGAAATGGCAGCGTCACTACGCCGAGAGCGCTGACTGGTCAGAGGACAGCGG 2180
 QY 673 gPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnTh 693
 Db 2181 ATTGCTTGCCTTCAACATGAGGAGGAGCAACCAAGAGCGAGATCTACGTGGCTTCAACAC 2240
 QY 693 rSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgTrpGluProVa 713
 Db 2241 CAGTCACCTTCCGGTGGTGTGTTGGGCTTCCAGAGCGCTCTGGGTCCGATGGGAGCGGT 2300

QY 713 lValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAl 733
 Db 2301 GGTGGACACCGGCAAGGAGGACCATATGACTTCTCCATCCGATGGCTGCCAGATCGTC 2360
 QY 733 aLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTy 753
 Db 2361 TGTCAACGCTTACCAAGTCTCTCATTTCTCACTCAATCTCATCTATCTCTAGCTA 2420
 QY 753 rSerSerValIleLeuValLeuArgProAspVal 764
 Db 2421 CTCCTCCATCATCTTGTATTTGGCCCTGATGC 2454
 RESULT 3
 US-09-463-238-2
 ; Sequence 2, Application US/09463238
 ; Patent No. 6469230
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Elizabeth A
 ; APPLICANT: Smith, Alison M
 ; APPLICANT: Bustos Guillen, Regla
 ; APPLICANT: Martin, Catherine R
 ; APPLICANT: Plant Bioscience Limited
 ; TITLE OF INVENTION: Search Debranching Enzymes
 ; FILE REFERENCE: 97.118
 ; CURRENT APPLICATION NUMBER: US/09/463,238
 ; CURRENT FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: PCT/GB98/02280
 ; PRIOR FILING DATE: 1998-07-30
 ; PRIOR APPLICATION NUMBER: GB 9716185.5
 ; PRIOR FILING DATE: 1997-07-31
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 2706
 ; TYPE: DNA
 ; ORGANISM: Solanum tuberosum
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2641)
 ; OTHER INFORMATION: n = a o r g o r c o r t
 US-09-463-238-2
 Alignment Scores:
 Pred. No.: 0 Length: 2706
 Score: 3029,00 Matches: 546
 Percent Similarity: 81.57% Conservative: 78
 Best Local Similarity: 71.37% Mismatches: 113
 Query Match: 71.91% Indels: 28
 DB: 4 Gaps: 7
 US-09-674-817B-3 (1-764) x US-09-463-238-2 (1-2706)
 QY 10 TrpArgPro-----AsnAlaThrAlaGlyLysGlyValGlyGluVal 23
 Db 178 TGGAGAAATCGAGCTCTCAGTGTATAGCTCTGTTTCATAGTGCAGCTGGAGGTGG 237
 QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluGluAspGluPro 43
 Db 238 -----GTGAAGACTGGCGCTACTGCGTGGTGGAG-----AAGCGG 276
 QY 44 ValAlaGluAspArgTyrAlaLeuGlyValAlaCysArg-----ValLeuAlaGlyMet 61
 Db 277 ACGACGAA-----CGATGCTGTTTTCAGGTTTATCAGGAGAG 315
 QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81
 Db 316 CCATTGCGGTTTGGTGTCTACTGCGACAGATGGTGGTGAATTCGCTCTTTTTCAGG 375
 QY 82 GlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101
 Db 376 AATGCTACAGCTGTCTCTTTGCTTGTACATCTTTTCCGATTTCCTTCCAGAGAGAGTG 435


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; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463.238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (822, 826, 2707 and 2797)
; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-11

Alignment Scores:
Pred. ID No.: 0 Length: 2806
Score: 2923.00 Matches: 538
Percent Similarity: 80.23% Conservative: 79
Best Local Similarity: 69.96% Mismatches: 119
Query Match: 69.40% Indels: 33
DB: 4 Gaps: 9

US-09-674-817B-3 (1-764) x US-09-463-238-11 (1-2806)
QY 10 TrpArgPro-----AsnAlaThrAlaGlyysGlyValGlyGluVal 23
Db 241 TGGAGAAATCGAGGTCTTCAGTGGTAAATGCTGCTTGCATAGTGCAGCGTGGAGGTG 300
QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluAspGluPro 43
Db 301 -----GTGAGACTCGCGCTACTCGCGTGGTGGTGGAG-----AAGCCG 339
QY 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgVal-----LeuAlaGlyMet 61
Db 340 ACGACGGAA-----CGATGCTGTTGAGAGTTTATACGGGAAAG 378
QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSergly 81
Db 379 CCAITGCGTGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
QY 82 GlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101
Db 439 AATGCTACAGCTGCTACTCTTTGCTTGCATCACTCTTTCCGATTTACTCTGAGAGAGAGTG 498
QY 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPhe 121
Db 499 ACCGAGCAATTTCTCGATCTCTCTAGTAAATAAAGTGGAGATGATGGCATGTGTTTC 558
QY 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141
Db 559 CTTAAGGAGAGATTTTGAGATATGCTATATGCTTACAAATTTGATGGGAAATTTCTGCTCT 618
QY 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161
Db 619 GAAGAGGACACTTTTGACTCTTCCAGATAGTGTGGATCTTATGCCAAGGCTATA 678
QY 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAla 181
Db 679 GTAAGCAGAGAGAGATATGTTGATATTAGGGCCAGAGGATGATTTGGGCCCAATGGCT 738
QY 182 GlyMetIleProLeuProTyr---SerThrPheAspTrpGluGlyAspLeuProLeuArg 200
Db 739 GGCATGGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 798
QY 201 --TyrProGlnLysAspLeuVal-IleTyrGluMetHisLeuArgGlyPheThrLysHis 219
Db 799 GTTTCACACAGAGAGATCTTGTTCATCNCATGAAATGATGCTGCTGGGTTTACTATCCAT 858

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QY 220 AspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyr 239
Db 859 GAGTCGAGTGAACAAATATCTGGTACTTACTCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 918
QY 240 LeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeu 259
Db 919 TTGAAGGAACCTTGGTGTCAACTGTATAGAGCTAATGCCCTGTACAGAGTTCATAGAGCTG 978
QY 260 GluTyrSerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSer 274
Db 979 GAGTACTATAGTATTAACCTCTGATTGGGCGACTACAAGTTTAACTTTTGGGGCTATCT 1038
QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294
Db 1039 ACTGTCAATTTCTTTTCTCCAAATGGGAAGATATCTCTGCTGGTCTAAGTAAATTCGCGC 1098
QY 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314
Db 1099 CTCGGTCCAAATAACGAATTAAGTATCTTGTCAAGAGAGCACATAAAGCTGGAATCGAG 1158
QY 315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334
Db 1159 GTTATCATGATGTGTTTCAATCACACTGCTGTAAGGAAATGAAATGCTCCCATCTATA 1218
QY 335 SerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr 354
Db 1219 TCATTAGAGGCAATGACACAGCTGTTTATACGCTAGCTCTTAAGGCTGAATTTTAC 1278
QY 355 AsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIle 374
Db 1279 AACTACTCAGAGTGTGGAATATCTTCAACTGTGTAATATCCCAATGCTAGCTCAATTTATA 1338
QY 375 ValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu 394
Db 1339 GTG---ATGCTGAGATATTTGGTTACCGAAATCGACGTACATGGCTTCGCTTTCATCTT 1395
QY 395 AlaserIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPro 414
Db 1396 GCTTCTATCTCTACAAAGAGTAGCAGCTCGTGAATGCTGTAAATGCTCTATGAAATTTCA 1455
QY 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProLeuIleAspMet 434
Db 1456 ATTGACGGTGAAGTATCACCACAGGCACTCTCTCACAGGCCCATGATGATGATG 1515
QY 435 IleSerAsnAspProIleLeuGlyValLysLeuIleAlaGluAlaTrpAspAlaGly 454
Db 1516 ATTAGCAATGATCCAATACTCTGTGGAGTAAAGCTTATAGCTGAAGCATGGGATTTGGA 1575
QY 455 GlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474
Db 1576 GGCTTTTACCAAGTTGGCATGTTTCCGCACTGGGTATCTGTCGGAGTGGACGGAAG 1635
QY 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAla 494
Db 1636 TACCGTGACATGTGTAGCGGCACTCATCAAGGCACTGATGGGTTTCTTGGGGCTTTTCT 1695
QY 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyValGlyArgGlyProTrpHisSer 514
Db 1696 GMAATGCTTTGTGGAGGCCCAATCTATACCAAGAGGAGGAGGAGAACCATGGACAGT 1755
QY 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534
Db 1756 ATAAATTCGTGTGTCGCCACCATGTTTACTTTTGGCTGATTTAGTGACATACACCAAT 1815
QY 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGlyAsnHisAsnLeuSerTrp 554
Db 1816 AAACAAATTTGCAATTTGGAGGAGCACAAAGACGGGAGAAATCAAAATAATAGTTGG 1875
QY 555 AsnCysGlyGluGluGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574
Db 1876 AATTGTGGTGGAGAGAGATTTTGAAGTATCTTGTGTAAGAAATTTGAGGAAAGACAA 1935

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QY 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
DB 1936 ATGCGGAACTTCTCTGCTGCTTATGCTTCCCAAGGTGTTCCATGATATATATGGC 1995
QY 595 AspGluTyrGlyHisThrLysGlyAsnAsnAsnThrTyrCysHisAspSerTyrVal 614
DB 1996 GATGATATGTCACACTTACGGGAGGAAACACACACGATATGCCATGATAATATAT 2055
QY 615 AsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633
DB 2056 AATTACTTCCCTGGGATAAGAGGATGAATCTTCACTGATTTTTCAGATTTTGGCGC 2115
QY 634 LeuMetThrLysPheArgLysGluCysGluCylLysLeuGlyLeuGluAspPheProThrAla 653
DB 2116 CTCATGACCAATTCGGCCATGAAATGTAATCACTGGGATTAGATGTTTCCCTACAGCA 2175
QY 654 LysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArg 673
DB 2176 GAAAGGCTGCAATGGCATGTCACACTCCAGACTCCAGATGGTCTGAAACAGTCGA 2235
QY 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThr 693
DB 2236 TTCCTTGCAATTCACACTGGTCGACAAAGTGAATCACTGGGATTAGATGTTTCCCTACAGCA 2295
QY 694 SerHisLeuProAlaValGluLeuProGluArgAlaGlyArgTyrProGluProVal 713
DB 2296 AGCAATTTGCTGTAAACGATTACACTTCCAGATAGGCTGTTATAGATGGACCGCTT 2355
QY 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733
DB 2356 GTGACACAGCAAAACAGCACCATTTCCTTGTACAGCAGCGTTCCTGAGAGAG 2415
QY 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753
DB 2416 ACAGCACCAAAACAAATATTTCTCAATTTCTGACGCGAACCAGTATCCGATCAGTTAT 2475
QY 754 SerSerValIleLeuValLeu 760
DB 2476 TCATCCATTATCTTTTACTA 2496

RESULT 5

US-09-187-124-1
; Sequence 1, Application US/09187124A
; Patent No. 6255563
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/187,124A
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: PCT/EP97/02292
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: DE 196 18 125.9
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1819)
; OTHER INFORMATION: Clone: Iso5
US-09-187-124-1

Alignment Scores:

Fred. No.: 2,1e-291 Length: 2133
Score: 2612.00 Matches: 460
Percent Similarity: 86.86% Conservative: 62
Best Local Similarity: 76.54% Mismatches: 73

Query Match: 62.01% Indels: 7
DB: 3 Gaps: 2

US-09-674-817b-3 (1-764) x US-09-187-124-1 (1-2133)

QY 166 GluTyrGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAlaGlyMetIlePro 185
DB 1 GAATTCGGCAGGAGCCAGAGGAT--GATTGTTGGCCCCCAATGGCAGGATGGTACCT 58
QY 186 LeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyrProGlnLysAsp 205
DB 59 TCTGCTTCTGATCAGTTTTCATTGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGAT 118
QY 206 LeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu 225
DB 119 CTGTGAATCTAGAAATGCAATGTTTGTGGATTTCAAATCATGAGTCGAGTGAACAAAA 178
QY 226 HisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyVal 245
DB 179 TATCCTGGTACTTACCTTGGTGTGTGGAGAACTTTCATCACTTGAAGGAACCTTGGTGC 238
QY 246 AsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer 265
DB 239 AACTGTATAGACTAATGCCCTGTCCAGATTTCAATGAGCTGAGTACTATAGTTATAAC 298
QY 266 Ser-----LysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSer 280
DB 299 TCTGATTGGGGCAGCTACAAAGTTTAACTTTTGGGGCTATTCTACTGTCAATTTCTTTCT 358
QY 281 ProMetThrArgTyrThrSerGlyCylLysAsnCysGlyArgAspAlaIleAsnGlu 300
DB 359 CCAATGGGAAGATATCTGCTGCTGCTAAAGTAAATTCGGCGCTCGGTGCAATAACGAA 418
QY 301 PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320
DB 419 TTTAAGTATCTGTCAAGGAACCATTAACGTGAATCGAGTTATCATGATGTTGTT 478
QY 321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp 340
DB 479 TTCAATCACACTGCTGAAGGAAATGAAATGTCCTACTATCATTTAGAGGCATTCAC 538
QY 341 AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360
DB 539 AACAGTGTGTTTATACGCTAGCTCCTAAGGGTGAATTTTACAACTACTCAGGATGTGA 598
QY 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
DB 599 AATACCTTCAACTGTATAATATCCCATTTGATCGTCAATTTATAGTGGATTGCTTGAAT 658
QY 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
DB 659 TGGGTTACCGAAATGCACGTAGATGGCTTCGCTTTGATCTTGTCTTCTATCTTACAGA 718
QY 401 GlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
DB 719 AGTAGCAGCTCGTGAATGCTGTAATGTCTATGGAATTCAAITGACGGTGACATGATC 778
QY 421 ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle 440
DB 779 ACCAGGCACCTCCTCAAAAGCCACCATTGATTGATATGATTAGCAATGATCCAAATA 838
QY 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGluValGly 460
DB 839 CTTAGTGGATTAAGCTTTTAGCTGAAGCATGGGATTGTGAGGCCCTTTTCAAGTTGGC 898
QY 461 GlnPheProHisThrAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArg 480
DB 899 ATGTTTCCGCACTGGGTATCTGTCGAGTGGAAACGGAAGTACCGTGACATGGTACGT 958
QY 481 GlnPheIleLysGlyThrAspGlyPheAlaGlyCylPheAlaGluCysLeuCysGlySer 500
DB 959 CAGTTTCATCAAGGCACTGATGGGTTTCTGGGGCTTTTCTGTAATGCCCTTTTGGGAAGC 1018

501 ProHisLeuTyr-GlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAla 520
1019 CCAATCTATACCAAGAGGAGGAGAGAAACCATGGAACATATAAATTCGTGTGTC 1078
521 HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn 540
1079 CACGATGGTTTACTTTCGTGCTGATTTAGTGACATACAAACAATAAACAACAATTTGGCAAT 1138
541 GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly 560
1139 CGAGGAGCAACAAGATGGGAGGAGATCACATAATAGTTGGAATTTGGCGAGGAGGA 1198
561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580
1199 GAATTGCAAGTATCTTTGTGAAGAAATTTGAGAAAGACAAATGCGGAATCTTCTCTC 1258
581 CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr 600
1259 TGCCTATGTTTCCCAAGGTTCCTCATGATATATATATATATATATATATATATATATAT 1318
601 LysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAsp 620
1319 AAGGAGGAGAAACAACAACGATTTGCGCATGACAAATATATATATATATATATATATATAT 1378
621 LysLys---GluGlnTyr-SerGluLeuHisArgPheCysCysLeuMetThrLysPheArg 639
1379 AAGAAGGATGATCTTCTCATCTGATTTTGTGATTTTGGCGCTCATGACCAATTCGCG 1438
640 LysGluCysGluGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHis 659
1439 CATGATGTGAATCACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498
660 GlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMet 679
1499 GGTCACTCTAGAACTCCAGATGGTCTGAAACAGTCAGTTCGTGATTTACACTG 1558
680 LysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaVal 699
1559 GTGCACAAAGTGAAGGAGAGACTATATATGCTTTTAAACGCCAGCCATTTGCTGTAACG 1618
700 ValGluLeuProGluArgAlaGlyArgTrpGluProValValAspThrGlyLysPro 719
1619 ATTACACTTCCAGAAAGCCTGGTATAGATGGCAGCGGTTTGGACACAGCAACCA 1678
720 AlaProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739
1679 GCACCATTTGACTTCTGACAGCAGATGTTCTCTGAGAGAGAGACAGCAGCAACAATAT 1738
740 SerHisPheLeuTyr-SerAsnLeuTyr-ProMetLeuSerTyrSerSerValIleLeuVal 759
1739 TCTCATTTCTGAGCGGACAGTATCCGATGCTCAGTATTCATCCATATATCTTTTA 1798
760 Leu 760
1799 CTA 1801

RESULT 6

US-09-850-936-1
Sequence 1, Application US/09850936
Patent No. 6670525
GENERAL INFORMATION:
APPLICANT: Emmermann, Michael
TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
TITLE OF INVENTION: FROM POTATO
FILE REFERENCE: GFB8
CURRENT APPLICATION NUMBER: US/09/850.936
PRIOR FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US/09/187.124
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/EP97/02292
PRIOR FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: DE 196 18 125.9

PRIOR FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2133
TYPE: DNA
ORGANISM: Solanum tuberosum
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1819)
OTHER INFORMATION: Clone: Iso5
US-09-850-936-1
Alignment Scores:
Pred. No.: 2,1e-291 Length: 2133
Score: 2612.00 Matches: 460
Percent Similarity: 86.86% Conservative: 62
Best Local Similarity: 76.54% Mismatches: 73
Query Match: 62.01% Indels: 7
DB: 4 Gaps: 2

US-09-674-817B-3 (1-764) x US-09-850-936-1 (1-2133)

166 GluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIlePro 185
1 GAAATTCGCGCAGGAGGCGCAGAGGAT--GATTGTTGGCCCCCAATGCGAGCATGTGACT 58
186 LeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAsp 205
59 TCTGCTTCTGATCAGTTTGTATGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGAT 118
206 LeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu 225
119 CTGTAATCTATGAAATGCAATGTCGTGGATTACAAATCATGAGTCGAGTGAACAAAA 178
226 HisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyVal 245
179 TATCCTGGTACTTACCTTGTGTGTGGAGAACTTGTATGAGTCACTTGAAGAACTTGGTGC 238
246 AsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSer 265
239 AACTGTATAGAGTAAATGCTGTCAGAGTTCATAGAGTCGAGTACTATAGTTATAAC 298
266 Ser-----LysMetAsnPheTrpGlyTyrSerThrIleAsnPheSer 280
299 TCTGATATGGCGCAGTACAAAGTTTAACTTTGGGGCTATCTACTGTCAATTTCTTTCT 358
281 ProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGlu 300
359 CCAATGGGAAGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
301 PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320
419 TTTAAGTATCTTGTCAAGGAGACATAAAGCTGGGAATCGAGTTTATCATGATGTTGTT 478
321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp 340
479 TTCAATCACACTGCTGAAGGAATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
341 AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360
539 AACAGTGTGTTTATACGCTAGCTCTCTAAGGGGTGAATTTTCAACTACTCAGAGTGTGGA 598
361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
599 AATACCTTCACTGTAATAATCCATGTCAGTCAATTTATAGTGGATTGCTTGATAT 658
381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
659 TGGGTTACCGAAATGACACGTAGATGCTTCCCGCTTGTGATCTTGTCTTATCTTCAAGA 718
401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420

Db 719 AGTAGCAGCTCGTGAATGCTCTAAATGCTATGCAAAATTCATTAAGTGGTGCATGATC 778
QY 421 ThrThrGlyThrProLeuValThrProProLeuLeuAspMetIleSerAsnAspProile 440
Db 779 ACCACAGGACCTCTCTCAACAGCCACCATTTGATATGATGATGATGATGATGATGATGAT 838
QY 441 LeuGlyGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 460
Db 839 CTTAGTGGAGTAACTTATAGCTGAGCATGGGATTTGTGGAGCCCTTACCAAGTTGGC 898
QY 461 GlnPheProHisThrAsnValTrpSerGluTrpAsnGlyLysTrpArgAspIleValArg 480
Db 899 ATGTTTCCGCACCTGGGTATCTGCTGGAGTGGAAAGGAAAGTACCCTGCATCGTACGT 958
QY 481 GlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySer 500
Db 959 CAGTTTCATCAAGGACCTGATGGGTTTTCGGGCTTTTGTGAATGCCCTTTGGGAGC 1018
QY 501 ProHisLeuTrpGlnAlaGlyLysArgLysProTrpHisSerIleAsnPheValCysAla 520
Db 1019 CCAAAATCTATACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1078
QY 521 HisAspGlyPheThrLeuAlaAspLeuValThrTrpAsnLysLysTrpAsnLeuProAsn 540
Db 1079 CACGATGGTTTACCTTGGCTGATTTAGTGACATACACAAATTAACCAATTTGGCAAT 1138
QY 541 GlyLeuAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly 560
Db 1139 CGAGAGGACACAAAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1198
QY 561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580
Db 1199 GAATTTGCAAGTATCTTTGTGAAGAAATGTGAGAAAGACAAATGCGGAACTTCTTCCCTC 1258
QY 581 CysLeuMetValSerGlnGlyValProMetPheTrpMetGlyAspGluTrpGlyHisThr 600
Db 1259 TGCCTTATGGTTTCCCAAGGCTTCCCATGATATATATGCGGTGATGATGATGATGATGAT 1318
QY 601 LysGlyGlyAsnAsnThrTrpCysHisAspSerTrpValAsnTrpPheArgTrpAsp 620
Db 1319 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1378
QY 621 LysLys--GluGlnTrpSerGluLeuHisArgPheCysCysLeuMetThrLysPheArg 639
Db 1379 AAGAAGGATGATCTTCATCTGATTTTGTGAGATTTTGGGCTTCATGACCAAAATCCGC 1438
QY 640 LysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHis 659
Db 1439 CATGAATGTGAATCACTGGGATAGATGTTTCCCTACAGCAGAAAGGCTGCAATGGCAT 1498
QY 660 GlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMet 679
Db 1499 GGTCACTCTTAGAATCCAGATTTGGTCTGAACAGCTCGATTCGTTGATTTACACTG 1558
QY 680 LysAspGluArgGlnGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 699
Db 1559 GTCCGACAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1618
QY 700 ValGluLeuProGluArgAlaGlyArgTrpGluProValValAspThrGlyLysPro 719
Db 1619 ATTACACTCCAGAAAGCGTGTATAGATGGCAGCGGTTTGTGGACAGGAGGAGGAGGAGGAG 1678
QY 720 AlaProTrpAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739
Db 1679 GCACCAATTTGACTTCTCTGACAGACGATGTTCTGAGAGAGAGAGAGGAGGAGGAGGAGGAG 1738
QY 740 SerHisPheLeuTrpSerAsnLeuTrpProMetLeuSerTrpSerValIleLeuVal 759
Db 1739 TCTCATTTTCTGGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1798
QY 760 Leu 760
Db 1799 CTA 1801

RESULT 7

US-09-463-238-3
; Sequence 3, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Alison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463,238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-09-463-238-3

Alignment Scores:

Pred. No.: 1,55e-171 Length: 2634
Score: 1577.00 Matches: 329
Percent Similarity: 58.90% Conservative: 111
Best Local Similarity: 44.04% Mismatches: 235
Query Match: 37.44% Indels: 72
DB: 4 Gaps: 19

US-09-674-817B-3 (1-764) x US-09-463-238-3 (1-2634)

QY 30 AlaAlaThrLysValGluAspGluGluAspGluProValAlaGluAspArgTyr 49
Db 239 GCAGCAGCTAACTTCAGGAGAGAGCT-----CCTCAATGCTGCACACTTTC 286
QY 50 AlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAla 69
Db 287 CCT-----TCATTCAAAAGTTTCCCTGCTGCTCATCCACTAGGAGTATCAGAA 337
QY 70 LeuAlaGlyGlyValAsnPheAlaValTrpHisValPheIleGluGlyGluLeu 89
Db 338 ACTGAAAGTGAATAAATTTTGCATTTTCTCAGCATGCTTCTGCAGTTTACACTTTC 397
QY 90 LeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAspPro 109
Db 398 ATAATTCTTCCAAAGAGAGTTCATGATGGAATGATT-----GAATTAGCATTTGGATCCA 451
QY 110 LeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeu-----His 127
Db 452 CAGAGAACCGCAGAGGAGCATATGGCATATGCAATTAAG---GAGTTGCCCAAGGT 508
QY 128 AsnMetLeuTrpGlyTrpArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeu 147
Db 509 GGTGTCCTTTATGTTATCGCATTTGATGACCTCGAAATGGCATGAAGGCGATCGATT 568
QY 148 AspValSerAsnValValAspProTrpAlaLysAlaValIleSerArgGlyGluTyr 167
Db 569 GATGATAGCATTTTGTGTTGATCCCTTACGCAAACTAATTTGAAGTCCAGCAGGTTT 628
QY 168 GlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPro 187
Db 629 GGA-----GATGAAAGCAATAAAATGTTAGATTGTTTGGCACTTATGATTTCAAT 679
QY 188 TyrSerThrPheAspTrpGluGlyAspLeuProLeu---ArgTyrProGlnLysAspLeu 206
Db 680 AGCTTGCCTTTTGTACTGGGAGAAATTTCAAGCTTCCAAATATATACCAGGAAAGATCTT 739

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Db      1748 AATGTGGAATTGAAGGTGAACCTTCAGATGCAAAATATTAAACCACTGGCTTCCACGGCAA 1807
Qy      575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
Db      1808 ATGAAAAATTTTCATTGGCAGCTGATGGTTCTCAGGGAACACCAATGATGCTTATGGGG 1867
Qy      595 AspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisaspserTyrVal 614
Db      1868 GATGAGTATGGGATACCCGCTATGGAATAATAACAGTTATGGATCATATACCGGCATC 1927
Qy      615 AsnTyrPheArgTirPaspLysLysGluGlnTyrSerGluLeuHis---ArgPheCysCys 633
Db      1928 AACAAATTCAGTGGGACAAATTGGAAGCAAGCAAGATGATCACTTCAGTTCTTTTTC 1987
Qy      534 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluaspPheProThrAla 653
Db      1988 AAGATGATAAGTTTCGACTGCCCAATGTTCTTAGAAAGGAAACCTTCATTGAGAAG 2047
Qy      654 LysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrp---SerGluAsnSer 672
Db      2048 AACGACATTAACCTGGCTC-----GAGGACAACTGGTACAAATAGAACTTGGTAG 2092
Qy      673 ArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluLurLeuTyrValAlaPheAsn 692
Db      2093 AGATTCTTCGATTATGCTCCATGATGGGAATGAGGAGATATTTACTTGGCATTTAAT 2152
Qy      693 ThrSerHisLeuProAlaValValGluLeuLeuProGlu---ArgAlaGlyArgArgTirpGlu 711
Db      2153 GCACACCACTTCCTCCATCAAAACAGCACTACCTTCACCAACCAGCAATAGAACTTGGTAC 2212
Qy      712 ProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAsp 731
Db      2213 CGAGTGTGGACACTAATCTGAAATCACCAGATGATTTGTACTGAGGAGTGCTCGT 2272
Qy      732 ArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeu 751
Db      2273 -----ATCAGTAAAACTTATGATGTTGGC 2296
Qy      752 SerTyrSerSerValIleLeu 758
Db      2297 CGGTACTCTGCTATCTCTT 2317

RESULT 8
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, f
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnos
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t

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NAME/KEY: misc feature	LOCATION: (600001)..(75000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (750001)..(900000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (900001)..(1050000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1050001)..(1200000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1200001)..(1350000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1350001)..(1500000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1500001)..(1650000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1650001)..(1800000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1800001)..(1950000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (1950001)..(2100000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2100001)..(2250000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2250001)..(2400000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2400001)..(2550000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2550001)..(2700000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2700001)..(2850000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (2850001)..(3000000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (3000001)..(3150000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (3150001)..(3300000)	OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature	LOCATION: (3450001)..(3600000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (3600001)..(3750000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (3750001)..(3900000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (3900001)..(4050000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (4050001)..(4200000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (4200001)..(4350000)	OTHER INFORMATION: n=a or c or g or t


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Db 447328 ATGATTCAATCAGGAGATGAGTATGCCCATACCGCGGAGCAATAACAACCGTTGGCT 447387
QY 610 HisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGlnTyrSerGluLeuHis 629
Db 447388 TTGGATTGGAATGCAATATCTCTTTGGATCAGCTTACCGCAAGCCATCAGCTGATG 447447
QY 630 ArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGluAsp 649
Db 447448 CACTTTCTCTGTATCTCAATTCGCTTTCGAAAAAATAATAAACACATTTTAAATCGAGGC 447507
QY 650 PheProThrAlaLysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAspTyrSer 669
Db 447508 TTCTTTCCATAAGGAATCAGTTGGGTAGATGCTATGGGAAATCCCATGACATGCGCG 447567
QY 670 GluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrVal 689
Db 447568 CCTGGAAT--TTCATTAGCATTTAAATAAATCGCAAAA--GGCATGTATATGTT 447621
QY 690 AlaPheAsnThrSerHisLeuProAlaValGluLeuProGlu 704
Db 447622 GCATTTCCGTGGAGCTCAAGCAACCTTGCACCTTACCTAAA 447666

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 3.3e-125 Length: 4403765
Score: 1225.00 Matches: 280
Percent Similarity: 51.41% Conservative: 85
Best Local Similarity: 39.44% Mismatches: 263
Query Match: 29.08% Indels: 82
DB: 3 Gaps: 19

US-09-674-817B-3 (1-764) x US-09-103-840A-2 (1-4403765)

QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyValAsnPhe 76
Db 1771671 GTGTGCCGGCGCAACGCCCTATCCGCTTGGAGCCACCTACGACGCGCGGACCACTTT 1771612
QY 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeu 96
Db 1771611 TCGTTGTTCCGAGATCGCCGAGAGGTGCGACTATGCTG-----ATC 1771567
QY 97 LysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsn 116
Db 1771566 GACGAGGACGGCGTCGAGTCGCGGATCCCGCTTGACGAGGTG-----GACGGGTAC 1771516
QY 117 ValTrpHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAsp 136

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Db 1771515 GTTCGCATGCCTATCTGCGGAACATCACCCCGCGCCAGCGCTACGGGTTTCGTGTGCAC 1771456
QY 137 GlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValValAspPro 156
Db 1771455 GGGCGGTTTCAGCCCGCGCGCCATCGGTGTGACCCAGCAAGCTGCTGTCGACCGC 1771396
QY 157 TyrAlaLysAlaValIleSerArgGlyGluTyrGly----- 168
Db 1771395 TATGGAGTCTTCCACGGCGATTTACCTTCGGGCGAGGCGCTGTATTCCTATGACGTC 1771336
QY 169 -----ValProAlaArgGlyAsnAsnCysTyrProGlnMetAla 181
Db 1771335 AACGCGGTTCAGCCCGACAGCAGCACTCCCGCATGTGTCGCTCGTGGCCACACTATGACC 1771276
QY 182 GlyMetIleProLeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyr 201
Db 1771275 AGCGTCGTGATCAATCCGTTCT-----TTCGACTGGGATACGACCGGTGCGCGCGCACC 1771222
QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLys---HisAsp 220
Db 1771221 CGGTACACAGAGACCGTAACTACGAAGCGCATGTCAAAGGCATGACACAGACCCATCCC 1771162
QY 221 SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys-----LeuAsp 238
Db 1771161 AGTATCCCGCCGAACTCCGGGCGCACCTACGCGCGCCTTGGCCGCCACCCCGGTGATCATCGAC 1771102
QY 239 TyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGlu 258
Db 1771101 CACCTCAACGAGTCAACGTCACCGCCCTTGAGTTGATGCGGTGCACAGTTCCTACAC 1771042
QY 259 LeuGluTyrSerThrSerSerLysMetAsnPheTyrGlyTyrSerThrIleAsnPhe 278
Db 1771041 GACTCCCGGCTGCTGGACCTCGGCTTGCAGAACTACTGGGTTCACACACCTTCGGAITC 1770982
QY 279 PheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIle 298
Db 1770981 TTCGCCCGCCACCACCATCAATACGCTCG-----ACCCGCGAAGCGCGC---AGCCGGTA 1770931
QY 299 AsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAsp 318
Db 1770930 GCGGAGTTCAAAACCATGTCGCGAGCTGCACGAAGCGGCATCGAGGTTCATCCTCGAC 1770871
QY 319 ValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGly 338
Db 1770870 GTGCTCTACACACACCGCTGAAGGCAACCACTTGGGTCCGACGATCAACTTTCGCGGA 1770811
QY 339 ValAspAsnThrThrTyrTyrMetLeuAlaProLysGly---GluPheTyr---AsnTyr 356
Db 1770810 ATCGACAACACCGCCTACTACCGACTGATGGACACGACTTGAGGTTCTCAAGGACTTC 1770751
QY 357 SerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAsp 376
Db 1770750 ACCGGTACCGGCAACAGCCTCAATGCCCGCCACCCACACACCTCGAGTGCATGATGAT 1770691
QY 377 CysLeuArgTyrTyrValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396
Db 1770690 TCGTTCGCTACTGGGTGATCGAAATGCACCTCAGCGGTTCCGTTTCGACTGGCGTCC 1770631
QY 397 IleMetThrArgGlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGlu 416
Db 1770630 ACCTGGCGCCGAGCTGCACGACGTCGCGGCTGCGGCATTC----- 1770586
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSer 436
Db 1770585 -----TTCGATCTCGTGCAA 1770571
QY 437 AsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---Gly 455
Db 1770570 CAAGATCCGGTGGTCAGTCAGTCAAGTGCATGCCGAGCCATGGGATGTCGGCGAAGGT 1770511
QY 456 LeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyr 475
Db 1770510 GGCTACAGGTTGGCAATCCCA-----GGACTGTGGAGGAATGGAACGCAAGTAC 1770457

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		; SEQ ID NO 1		LENGTH: 4411529	
		; TYPE: DNA			
		; ORGANISM: Mycobacterium tuberculosis			
		; OTHER INFORMATION: H37Rv			
		US-09-103-840A-1			
		Alignment Scores:			
		Pred. No.:		3.31e-125	
		Score:		1225.00	
		Percent Similarity:		51.41%	
		Best Local Similarity:		39.44%	
		Query Match:		29.08%	
		Dbs:		3	
		US-09-674-817B-3 (1-764) x US-09-103-840A-1 (1-4411529)			
Qy	57	ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyValAsnPhe	76		
Db	1771545	GTGTGGCGGGCAACGGCTATCCGCTTGGAGCCACCTACGACGGCGCGGACCACTTT	1771486		
Qy	77	AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeu	96		
Db	1771485	TCGTGTCTCCGAGATCGCGGAGAGGTGAGTATGCTCTG-----ATC	1771441		
Qy	97	LysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsn	116		
Db	1771440	GACGAGGACGGCGTCGAGTCGCGGATCCGCTTACGAGGTG-----GACGGGTAC	1771390		
Qy	117	ValTrpHisValPheIleGluGlyLeuHisMetLeuTyrGlyTyrArgPheAsp	136		
Db	1771389	CTCTGGCATGCTATCTCCGCAACATCACCCCGCGGCGCTACGGGTTCGTGTGCAC	1771330		
Qy	137	GlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAspPro	156		
Db	1771329	GGCGGTTCGACCGCGGGCGGCATCGGTGTGACCCCGCAAGCTGCTGCTGACCGG	1771270		
Qy	157	TyrAlaLysAlaValIleSerArgGlyGluTyrGly-----	168		
Db	1771269	TATGGAGATGCTTCCACGGCGATTTTCCCTTCGGCGAGCGCTGTATTCTCTATGACGTC	1771210		
Qy	169	-----ValProAlaArgGlyAsnAsnCysTrpProGlnMetAla	181		
Db	1771209	AACGCGCTGACCGCGACAGCAGCTCCCGATGTGTGCTGCTGCGGCCACACTATGACC	1771150		
Qy	182	GlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyr	201		
Db	1771149	AGCGTCGTGATCAATCCGTTT-----TTCGACTGGGCATACGACCGGTGCGCGCACC	1771096		
Qy	202	ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLys---HisAsp	220		
Db	1771095	CGGTACACGAGAGCGTAATCTAGAGCGCATGTCAAGCGATGATGACAGACCATCC	1771036		
Qy	221	SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys-----LeuAsp	238		
Db	1771035	AGTATCCCGCGCAACTCCGGCGCACCTACGCGCGCTGGGCCACCGGTGATCATCGAC	1770976		
Qy	239	TyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGlu	258		
Db	1770975	CACCTCAACGAGCTCAACGTCTCAGGTTGATGCGCGGTGACCGGTCTCTACAC	1770916		
Qy	259	LeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhe	278		
Db	1770915	GACTCCCGGTGCTGGACCTCGGCTTGGAACTACTGGGTGTACACCTTCGGATTC	1770856		
Qy	279	PheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIle	298		
Db	1770855	TTCCGCGCGCACCATCAATACCGCTCG-----ACCGCGAAGCGCGG---AGCGCGGTA	1770805		
Qy	299	AsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAsp	318		
Db	1770804	GCCGAGTTTCAAAACCATGCTGCGGAGCCTGCGACGAGCCGATCGAGTTCATCTCGAC	1770745		

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

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QY 319 ValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGly 338
Db 1770744 GTCGCTACACACACACCGCTGAAGCAACACCTTGGTCCGACGATCACTTTCGGGA 1770685
QY 339 ValAspAsnThrThrTyrTyrMetLeuAlaProLysGly---GluPheTyr---AsnTyr 356
Db 1770684 ATCGACAAACCGCTACTACCGACTGATCGACACCGACTTGAGTTCTACAAGGACTTC 1770625
QY 357 SerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAsp 376
Db 1770624 ACCGGTACCGGCAACACGCTCAATGCGCGCACCCACACACCCCTGCAGCTGATCATGGAT 1770565
QY 377 CysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396
Db 1770564 TCGCTGCGCTACTCGGATGATCGAATTCACGCTGACGGTTCGGTTTCGACCTGGCGTCC 1770505
QY 397 IleMetThrArgLysSerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGlu 416
Db 1770504 ACGTGGCCCGCGAGCTGACGAGCTGACCGGCTGTCGCAATTC----- 1770460
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProLeuLeuAspMetIleSer 436
Db 1770459 -----TTCGATCTGGTGCA 1770445
QY 437 AsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---Gly 455
Db 1770444 CAAGATCCGCTGCTCAGTCAGGTCAGCTGATCGCGAGCCATGGGTGTCGCGAGGT 1770385
QY 456 LeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyr 475
Db 1770384 GGGTACAGGTTGGCACTTCCCA-----GGACTGTGCGGAATGGAACGCAAGTAC 1770331
QY 476 ArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGlu 495
Db 1770330 CGGACACCGTGGCGACTACTGGGAGGCGAGCCGCCACCTAGCGCAATTCGGCTCC 1770271
QY 496 CysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIle 515
Db 1770270 CGGCTACCGCGGTCGTCGGACCTCTACGAAGCAACCGCGCGCCGCGCCAGTATC 1770211
QY 516 AsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLys 535
Db 1770210 AATTTGTCACCGCCACGACGGGTTCACTCAACGACTGTGTCTCGTACACGACAAG 1770151
QY 536 TyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsn 555
Db 1770150 CACAACGAGGCCAATGGCGAGAACACCGCGACGCGGGAAGCTACACCGATCGTGGAC 1770091
QY 556 CysGlyGluGlyGlnPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMet 575
Db 1770090 TGGCGGTGTCAGGCGCCCAACCGATGATGACCCCGACATCTTGGCGTGGCTGCCCGCCAGATG 1770031
QY 576 ArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAsp 595
Db 1770030 CGCAACATGTGGCGCCAGCTTATGTTGTCAGCGGCGACCGCGATGATCCGCCACGCGAC 1769971
QY 596 GluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsn 615
Db 1769970 GAGATTGGGCGCACCAATACCGCAACAAACGCTCTACTGCCAGGACTCCGAATTTATCT 1769911
QY 616 TyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMet 635
Db 1769910 TGGATGATTGGTCATTGGTGGCAAGAATGCGATCTCTAGCTTTCGCACGCAAGGCG 1769851
QY 636 ThrLysPheArgLysGlu-----CysGlnGlyLeuGly 646
Db 1769850 ACGACCTTGGCAAGAACCAACAGGTGTTTCGCGGACGCGGTTCTTTGAGGGTGAACCG 1769791
QY 647 LeuGluAspPheProThrAlaLysArgLeuGlnTrp-----HisGlyHisGlnPro 663
Db 1769790 ATCCGAGTGGCGACGAAGTCCCGGATATCGCTGTTGACACCGGCGGTCGGGAGATG 1769731
QY 664 GlyLysProAspTrpSerGluAsn---SerArgPheValAlaPheSerMetLysAspGlu 682
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Db 1769730 ACGCAGGAGATTGGGGCAGAGGCTTCACAGGTGTGTGGGTCTTCTCAACGGTGAA 1769671

QY 683 -----ArgGlnGlyGlu-----IleTyrValala 690

Db 1769670 GCCATTACCGACCGAGCCCGGTGGTAGCGAGTAGTCGAGGATTATTCTCTGTGTTC 1769611

QY 691 PheAsnThrSerHisLeuProAlaValValGluLeuPro---GluArgAlaGlyArgArg 709

Db 1769610 TTCAACGCCCATGACACGAGCTGCGAGTTCGTGATCGCGCATGACGGCTATGCGGACGAG 1769551

QY 710 TrpGluProValValAspThrGlyLysPro 719

Db 1769550 TGGACCGGAGAGCTGGATACCAACGATCCC 1769521

RESULT 11:

US-09-129-075-3

Sequence 3, Application US/09129075

Patent No. 6087149

GENERAL INFORMATION:

APPLICANT: Teutsumi, No. 6087149siko

APPLICANT: Bisgaard-Frantzen, Henrik

APPLICANT: Svendsen, Allan

TITLE OF INVENTION: Starch Conversion Process

FILE REFERENCE: 5262.204-US

CURRENT APPLICATION NUMBER: US/09/129,075

CURRENT FILING DATE: 1998-08-04

EARLIER APPLICATION NUMBER: 0787/97

EARLIER FILING DATE: 1997-07-02

EARLIER APPLICATION NUMBER: 60/055,867

EARLIER FILING DATE: 1997-08-13

EARLIER APPLICATION NUMBER: PCT/DK98/00304

EARLIER FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

TYPE: DNA

LENGTH: 2181

ORGANISM: Rhodothermus marinus

US-09-129-075-3

Alignment Scores:

Pred. No.: 1,43e-126 Length: 2181

Score: 1187.00 Matches: 294

Percent Similarity: 50.26% Conservative: 86

Best Local Similarity: 38.89% Mismatches: 242

Query Match: 28.18% Indels: 134

DB: 3 Gaps: 30

US-09-674-817B-3 (1-764) x US-09-129-075-3 (1-2181)

QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPhe 76

Db 40 GTCTGGCCCGCGCGCTTATCCGCTGGTGCCACCTGGGACGGGCTGGGGCTCAACTTT 99

QY 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThr---ProGluAsp 95

Db 100 GCCCTCTACAGCCAGCAGCGCGAGCGGTGCAACTGGTGTCTTCGACCCACCGCGAGAT 159

QY 96 LeuLysAlaAspArgValThrGluValProLeuAspProLeuMetAsnArgThrGly 115

Db 160 CCGCGCGCTTCGCCACGATCGAA-----GTGACCGACGACGACGCG 201

QY 116 AsnValTrpHisValPheIleGluGlyLeuHisAsnMetLeuTyrGlyTyrArgPhe 135

Db 202 CCGATCTGGCATGTGTACCTGCGCGCGCTGGTCCCGCCGCGCTCTACGGCTATCGGCTC 261

QY 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAsp 155

Db 262 TACGACCCCTACCGCGCGGAGGAGGCGCGCTTCAATCCGAACAAGGTGCTGCTCGAC 321

QY 156 ProTyrAlaLysAlaValIleSerArgGlyGlyValProAlaArgGlyAsnAsn 175

Db 322 CCCTACGCGAAGCCATC-----GGCCGCCCCCTTCGC----- 354
Qy 176 CysTrpProGlnMet-----AlaGlyMetIleProLeu 186
Db 355 ---TGGACACAGCCCTCTCGGTTACAAAATCGCGATCCGCGCGGGATCTGTCTTC 411
Qy 187 -----ProTyrSer-----ThrPheAsp 192
Db 412 TCCGACAGACAGCGCTCCGTACGCGCCGCTGGAGCCGCTCGTGGAGGCTGTTCGAG 471
Qy 193 TrpGluCysAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHis 212
Db 472 TGGGGGACACCGCCCGCCGCGCATTCCTCGGAAGACACGATCATCTACGAACGGCAC 531
Qy 213 LeuArgGlyPheThrLysHisAspSerSerAsnValIleHisPro----- 227
Db 532 GTCAGGGCATCAGGAG-----CTGCATCCGGAAGTCGCGGAGCGC 573
Qy 228 -----GlyThrPheIleGlyAlaValSerLys-----LeuAspTyrIleLysGluLeu 243
Db 574 CTGCGGGGACGATCTCGGGGCTGACCTCGACCGCGGTCTGGACACCTGAAGCAGCTG 633
Qy 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263
Db 634 GCGGTACACGATCCAGCTCTCTCGGTGCACCAAAAGTCACGATCGGCACCTGGTC 693
Qy 264 SerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThr 283
Db 694 GAGCGCGGCTGGCGCACTACTGGGCTACAATCCGCTCTGTACTTTGCGCGGAGCC 753
Qy 284 ArgTyr---ThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLys 302
Db 754 GAGTACCCACGACGCGCCGATC-----TCGCGCTGCGCGATTCAG 798
Qy 303 ThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsn 322
Db 799 ATGATGTGCGGCGCTGCTGTCGCGGTTCGAGTGATCTCGACGTGCTACAAAC 858
Qy 323 HisThrIleGluGlyAsnGluAsnGlyProIleSerPheLysGlyValAspAsnThr 342
Db 859 CACACGGCGAAGCGCGCTGCTGGCGCCACCGCTCTGCTCGGGGCTATCGACAAACCGC 918
Qy 343 ThrTyrTyrMetLeuAlaProLysGlyGluPheTyr-----AsnTyrSerGlyCysGly 360
Db 919 GCCTACTACAGCCGATCCGACAAACCCCGCTTCTGTCGATTACAGGCGCACCGGC 978
Qy 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
Db 979 AACACGCTGGACGTGGCAACCCCTACGTCTACATCATCATGACACGCTTCGCTAC 1038
Qy 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
Db 1039 TGGGTCACTGAATGACGCTGACGCGTTTCGTTTCGACCTGCGCGCGCTGGCCCGC 1098
Qy 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
Db 1099 -----GAGCTGTACGACGTG-----GACATGCTC 1122
Qy 421 ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle 440
Db 1123 TCGACC-----TTTTTTCAGTCTCATTCAGACGACCGCGGTG 1158
Qy 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---GlyLeuTyrGlnVal 459
Db 1159 CTCAGCCAGGTCAAGCTCATCGCGAACCTCGGACGTGGCGCGCGGGGTATCAGGTG 1218
Qy 460 GlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleVal 479
Db 1219 GGACATTTTCCC---TGGCAG---TGGACGAGTGGAAACGGCGCTATCTGTGACGCGGTG 1272
Qy 480 ArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGly 499
Db 1273 CGCCGCTTCTGGCGGGGCGATCGGGGCTCAACGGTGAGTTTGCCACGCGCTTTGCGCGC 1332

Qy 500 SerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCys 519
Db 1333 TCCAGCGATCTGTACGAACGTAGCGGTCTGCTCGCTTCTCGATCAACTTCGTCAAG 1392
Qy 520 AlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuPro 539
Db 1393 GCGCACACGCGCTTTCACCTCGGAAGACCTGTGTAGCTTACGAAAGACACACGAGCG 1452
Qy 540 AsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlu 559
Db 1453 AATCTGGAAGCGACACCGGCGCATCGACGAAACTTACAGCACGAACCTCGCGGTGGAG 1512
Qy 560 GlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePhe 579
Db 1513 GGACCCACGCGAGTCCGTCTGCTGCGCGGAGCGGTCAAGCGCACGCTGATC 1572
Qy 580 ValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHis 599
Db 1573 AGCAGCTCTTCTCTCGAGGGGTGCCCATGTCTGGCGCGCGACGAGCTTCGCGC 1632
Qy 600 ThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyr 619
Db 1633 ACGCAGCAGCGCAACAAACGCTATTGCCAGGACAAACGAGATCAGCTGTACAACTGG 1692
Qy 620 Asp-----LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThr 636
Db 1693 CAGCTCGACACCGCAAGCAGCAGTCTCTGAG-----TTCGTGCCCGACGATC 1743
Qy 637 LysPheArgLysGluCysGlyGluGlyLeuGluAspPheProThrAlaLysArgLeu 656
Db 1744 TGGTTTCGACGACGATCGGAGCTTCGCGCGCGCATTTTCTGACCGGATTTGCCC- 1800
Qy 657 GlnTrpHisGlyHisGlnPro-----GlyLysPro----- 666
Db 1801 -----AACCGCGAAGCGCCCGACGAGTCTGGTGGCACCTGAGGTGCGCCATCGC 1854
Qy 667 -----AspTrpSerGluAsnSerArgPheValAlaPheSerMet----- 679
Db 1855 CACGAGGACTGAGCC---AACCGGAGCTGACGCGCTTCGACTGCTGTGTCACGGGAC 1911
Qy 680 -----LysAspGlu-----ArgGlnGlyGluIleTyrValAla 690
Db 1912 GCCATTTCAGGGGACCGACGACGACGAGCGTTCGCGACGACACGCTTCTGTGATTCTG 1971
Qy 691 PheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly----- 707
Db 1972 TCAACAACGCGACGAGCGAGCGTCCGCTGCTGCGGAGGTATGCTCCTGTGGCAAG 2031
Qy 708 ---ArgArgTrpGluProVal-----ValAspThrGlyLysProAla 720
Db 2032 CCGCACCACTGGAGGTGCTCCCGTGTTCACGCAATGTGGAGCCCCCAGCTGCGCGC 2091
Qy 721 ProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIle 736
Db 2092 CCGCGCGAGACGCTGTGCTG-----CTCCCGCGCGGTGTGACGCTG 2133

RESULT 12

US-09-346-237-12
; Sequence 12, Application US/09346237A
; Patent No. 6265197
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 5629.200-US
; CURRENT APPLICATION NUMBER: US/09/346.237A
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: PA 1998 00868
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: 60/094,353
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Rhodotermus marinus DSM 4252
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
; OTHER INFORMATION: IscAmylase
US-09-346-237-12
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Alignment Scores:

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Pred. No.: 1.43e-126 Length: 2181
Score: 1187.00 Matches: 294
Percent Similarity: 50.26% Conservative: 86
Best Local Similarity: 38.89% Mismatches: 242
Query Match: 28.18% Indels: 134
DB: 3 Gaps: 30
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US-09-674-817B-3 (1-764) x US-09-346-237-12 (1-2181)

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QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThraLeuAlaGlyValAsnPh 76
Db 40 GTCTGGCCCGCCGCGCTTATCCGCTGGGTGCCACCTGGACGGCGTGGCGTCAACTTT 99
QY 77 AlaValTyrSerGlyGlyAlaThraAlaAlaAlaLeuCysLeuPheThr----ProGluAsp 95
Db 100 GCCTCTACAGCCAGCGAGCGCGGTGGAATGGTGTCTGACACCCCGGAGCAT 159
QY 96 LeuYsAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115
Db 160 CCCCGCGCTTCGCGCACGATCGAA-----GTGACCGAAGCGGACGACGC 201
QY 116 AsnValTrpHisValPheIleGluGlyLeuHisAsnMetLeuTyrGlyTyrArgPhe 135
Db 202 CCGATCTGGATGTGATCTCCCGCGCTGCGTCCCGCGCAGCTCTACGGCTATCGCGTC 261
QY 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAsp 155
Db 262 TAGGACCTTACCGCGCGGAGGAGCCACCGCTTCAATCCGACACAGGTGCTGCTCGAC 321
QY 156 ProTyrAlaValAlaValIleSerArgGlyGlyValProAlaArgGlyAsnAsn 175
Db 322 CCCTACCGAAGGCCATC-----GGCGGCGCCCTTCGC-----354
QY 176 CysTrpProGlnMet-----AlaGlyMetIleProLeu 186
Db 355 ---TGGACGACAGCCTCTTCGGTTACAAATCGGCGATCCGCGGGATCTGTCTGTTTC 411
QY 187 -----ProTyrSer-----ThrPheAsp 192
Db 412 TCGAAGAGACAGCGCTCTCGTACGCGCGCTGGAGCGCTGCTGGAGGCGTGTTCGAG 471
QY 193 TrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHis 212
Db 472 TGGGGACACCGCGCGCGCATTCCTCGGGAAGACACGATCATCTACGAAACGCAC 531
QY 213 LeuArgGlyPheThrLysHisAspSerAsnValGluHisPro-----227
Db 532 GTCAAGGGCATCAGAG-----CTGCATCCGGAAGTGGCGGAGCGCG 573
QY 228 -----GlyThrPheIleGlyAlaValSerLys-----LeuAspTyrLeuLysGluLeu 243
Db 574 CTCGGGGGACGATCTGGGGCTGACCTCGAGAGCGCGTGTGAGCACCTGAAGCAGCTG 633
QY 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGlyTyrSerThr 263
Db 634 GCGGTACACGATCAGTCTCTCTCCGGTGCACCGAAAGTGCACGATCGGACCTGGTGC 693
QY 264 SerSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 694 GAGCGGGCGTGGCGCAACTACTGGGGCTACAATCCGCTCTGCTACTTTCGCGCGGAGCCC 753
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QY 284 ArgTyr---ThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLys 302
Db 754 GAGTACGCCACGACGAGCGCGATC-----TCGCCGTGGCGAGTTCAG 798
QY 303 ThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsn 322
Db 799 ATGATGTCGGCGCGCTGATGTCGGCGCTTCGAGGTGATGTCGACGCTGTCTACAAC 858
QY 323 HisThrAlaGluGlyAsnGlyProIleLeuSerPheLysGlyValAspAsnThr 342
Db 859 CACACGGCGAAGCGCGCTGGGCCCCACGCTGTCTCCGGGCGATCAGAACCCG 918
QY 343 ThrTyrTyrMetLeuAlaProLysGlyGluPheTyr-----AsnTyrSerGlyCysGly 360
Db 919 GCCTACTACAGCGCGATCCGAACACCGCGCTTCTGGTTCGATTACACGGCGACCGCG 978
QY 361 AsnThrPheAsnCysAsnHisProValArgGlnPheIleValAspCysLeuArgTyr 380
Db 979 AACACGCTGGACGTGGGCAACCCCTACGTCATCCAGCTCATCATGACAGCCCTGGCTAC 1038
QY 381 TrpValThrGluMetHisValAspGlyPheAspPheAspLeuAlaSerIleMetThrArg 400
Db 1039 TGGGTCACTGAAATGCAGTCCAGCGCTTTCGGTTCGACCTGGCGCGCGCTGGCGCGC 1098
QY 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
Db 1099 ---GAGCTGTACGAGCTG-----GACATGTCTC 1122
QY 421 ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle 440
Db 1123 TCGACC-----TTTTTTCAGGTCAATTCAGCAGGACCCGGTG 1158
QY 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---GlyLeuTyrGlnVal 459
Db 1159 CTCAGCCAGGTCAAGCTCATGCCGAACCTGGGACGTCGGCGCGGGGGGTATCAGGTG 1218
QY 460 GlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleVal 479
Db 1219 GGACATTTTCCC---TGGCAG---TGGACCGAGTGAACCGCGCTATCGTGAAGCCGCTG 1272
QY 480 ArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGly 499
Db 1273 CGCCGCTTCTGGCGGGCGATCGGGCGCTCAACGGTGTGAGTTTGCACCGCTTTCGCGGC 1332
QY 500 SerProHisLeuTyrGlnAlaGlyArgLysProTrpHisSerIleAsnPheValCys 519
Db 1333 TCCAGCGATCTGTACGAACGTAGCGGTGCTGCTCGCTTCGCTTCGATCACTTCGTTCAGC 1392
QY 520 AlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuPro 539
Db 1393 GCGCACGACGCGTTCACGCTGGAAGACCTGTGTAGCTACAGCAAAAGACCAACGAGCG 1452
QY 540 AsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlu 559
Db 1453 AATCTGGAAGCAACCGGCGATGACGAAACCTACAGCAGCAACTGCGGGGTGGAG 1512
QY 560 GlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePhe 579
Db 1513 GGACCCAGCAGGATCCGCTCGCTCGCTCGCGCTCGCGGGAAGCGCTCAAGCGCAGCTGATC 1572
QY 580 ValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGlyTyrGlyHis 599
Db 1573 AGCAGCTCTTCTCTCGCAGGGCTGCCCATGCTGTGGCGCGCGAGCTGTCGCGC 1632
QY 600 ThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrp 619
Db 1633 ACGCAGCGCGCAACCAACCGCTATTCGACGACCAACGAGATCAGCTGTGTACACTGG 1692
QY 620 Asp-----LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThr 636
Db 1693 CAGCTCGACAGCGCGCAGCAGCAGTTCCTGGAG-----TTCGTGCCCGCAGCAGATC 1743
QY 637 LysPheArgLysGluCysGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeu 656
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Db 1744 TGGTTCGCAAGCAGCATCGAGCTTCGGCGCGCGCCATTTCTGACCGGATTGCC--- 1800
 Qy 657 GlnTrpHisGlnPro-----GlyLysPro----- 666
 Db 1801 -----AACGGCGGAGGCGCCCGACGAGTCTGGTGGACCTGAGGGTGGCCCATGGCG 1854
 Qy 667 -----AspTrpSerGluAsnSerArgPheValAlaPheSerMet----- 679
 Db 1855 CACGAGGACTGGACC---AACCGGAGCTGACGGCTTCGGACTGCTGCTGCACGCGCAC 1911
 Qy 680 -----LysAspGlu-----ArgGlnGlyGluLeuValAla 690
 Db 1912 GCCATTACGGGAGCGGACGAGCAGCAGCCGTTTCGGGACGACACGTTTCTGATTCTG 1971
 Qy 691 PheAsnThrSerHisLeuProAlaValGluLeuProGluValArgAlaGly----- 707
 Db 1972 TTCAACACGCGCAGCGAGCGGTGGCGGTGCTGGTGGCGAGGTATGCTCTGTGGCAAG 2031
 Qy 708 ---ArgArgTrpGluProVal-----ValAspThrGlyLysProAla 720
 Db 2032 CCGCACCATCTGGAGGTGGTCCCGGTGTTTCAACGCAATGTGGAGCCCGCCACGTCGCG 2091
 Qy 721 ProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIle 736
 Db 2092 CCGCGGAGAGCGGTGTCTG-----CTCCCGCGGGGTGCTGACGGTG 2133

RESULT 13

US-09-544-123-3
 ; Sequence 3, Application US/09544123
 ; Patent No. 6448049
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsutsumi, No. 6448049iko
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Svendsen, Allan
 ; FILE OF INVENTION: Starch Conversion Process
 ; TITLE REFERENCE: 5262.204-US
 ; CURRENT APPLICATION NUMBER: US/09/544,123
 ; CURRENT FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 09/129,075
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 0787/97
 ; PRIOR FILING DATE: 1997-07-02
 ; PRIOR APPLICATION NUMBER: 60/055,867
 ; PRIOR FILING DATE: 1997-08-13
 ; PRIOR APPLICATION NUMBER: PCT/DK98/00304
 ; PRIOR FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 2181
 ; TYPE: DNA
 ; ORGANISM: Rhodothermus marinus
 US-09-544-123-3

Alignment Scores:
 Pred. No.: 1,43e-126 Length: 2181
 Score: 1187.00 Matches: 294
 Percent Similarity: 50.26% Conservative: 86
 Best Local Similarity: 38.89% Mismatches: 242
 Query Match: 28.18% Indels: 134
 DB: 4 Gaps: 30

US-09-674-817B-3 (1-764) x US-09-544-123-3 (1-2181)

Qy 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPhe 76
 Db 40 GTCTGGCGCGCGCGCTTATCCGCTGGGTGCCACCTGGGAGCGGCTGGGCGTCACTTT 99
 Qy 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThr---ProGluAsp 95
 Db 100 GCCCTCTACAGCAGCAGCGCGGCGGTGCAACTGGTGTCTGTTTCGACCCACCGCGAGAT 159

Qy 96 LeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115
 Db 160 CCGCGGCTTCGGCGCAGCATCGAA-----GTGACCGAACGACGAGGC 201
 Qy 116 AsnValTrpHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPhe 135
 Db 202 CCGATCTGGCATGTGTACTTCCCGGCTCGCTCCCGCAGCTCTACGGCTATCGGTC 261
 Qy 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAsp 155
 Db 262 TACGACCCCTACCGCGCGGAGGAGCCCGCTTCAATCCGACCAAGGTGCTGCTCGAC 321
 Qy 156 ProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsn 175
 Db 322 CCTTACGCGAAGGCATC-----GGCCGGCGCCCTTCGC----- 354
 Qy 176 CysTrpProGlnMet-----AlaGlyMetIleProLeu 186
 Db 355 ---TGGCAGCAGACAGCTCTTCGGTTACAAATCGCGCATCGCGCGGGATCTGTCTGTT 411
 Qy 187 -----ProTyrSer-----ThrPheAsp 192
 Db 412 TCCGAAGACAGCAGCGTCTCGTACCGCCGCTGGAGCCGCTGGAGGGCTGTTTCGAG 471
 Qy 193 TrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHis 212
 Db 472 TGGGGGAGCAGCGCCCGCGCATTCCTTGGGAGACACGATCATCTACGAAACGAC 531
 Qy 213 LeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPro----- 227
 Db 532 GTCAAGGGCATCAGCAAG-----CTGCATCCGGAAGTCCGCGAGCGCG 573
 Qy 228 -----GlyThrPheIleGlyAlaValSerLys-----LeuAspTyrLeuLysGluLeu 243
 Db 574 CTGCGGGGAGCATCTCGGGCTGACCTGCGAGCGGCTGCTGGAGCACCTGAAGCAGCTG 633
 Qy 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263
 Db 634 GCGGTCAACACGATCCAGCTCTTCCGGTGCACCAAAAGTGCAGTCCGCGCTGGTC 693
 Qy 264 SerSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThr 283
 Db 694 GAGCGCGCTTGGCAACTACTGGGCTACAATCCGCTCTGCTACTTTGCGCGGAGGCC 753
 Qy 284 ArgTyr---ThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLys 302
 Db 754 GAGTACGCGCACCAACGCGCGCATC-----TCGGCGGTGCGCGGAGTTCAAG 798
 Qy 303 ThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsn 322
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 Qy 323 HisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThr 342
 Db 859 CACACGGCGAAGGGCGGTGCTGGCGCCACCGTGTCTTCCGGGGCATCGACACCGC 918
 Qy 343 ThrTyrTyrMetLeuAlaProLysGlyGluPheTyr-----AsnTyrSerGlyCysGly 360
 Db 919 GCCTACTACAAGCGCGCATCCGGAACACCGCGCTTCTGCTGCGATTACCGGGCACCGCG 978
 Qy 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
 Db 979 AACACGCTGGAGCTGGGCAACCCCTACGTCATCCAGCTCATGTGACAGCGCTCGCTAC 1038
 Qy 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
 Db 1039 TGGGTCACTGAATAACGCTGACCGCTTTCGGTTCGACCTGGCGCGCGCGCTGCCCGC 1098
 Qy 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
 Db 1099 -----GAGCTGTACGAGCTG-----GACATGCTC 1122
 Qy 421 ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle 440

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DB CACAGCGAGGTCAAGCTCATCGCGAACCTCGGACCTCGGCGCGGGGGGTATCAGGTG 1218
QY GlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleVal 479
DB GGACATTTCC---TGGCAG---TGGACCGAGTGGACGGCCCTATCTGACCGCGTG 1272
QY ArgGlnPheIleLeuGlyThrAspGlyPheAlaGlyPheAlaGluCysLeuCysGly 499
DB CCGCGCTTCTGGCGGGCGGATCGGGCGCTCAACGCTGAGTTTGCACCGCGCTTTCGCGGC 1332
QY SerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCys 519
DB TCCAGCGATCTGTACAGCAGTAGCGTCTGCTCGTTCGTTCTGATCACTTCGTACG 1392
QY AlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuPro 539
DB GCGCACGACGGCTTCACGCTCGAAGACCTGGTCACTACACGAAAAAGCAACAGCAGCG 1452
QY AsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlu 559
DB ATCTGGAGGCAACCGGACGGCATGACGCAAACTACACACGAACTCGCGGGTGGAG 1512
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QY GlnTrpHisGlyHisGlnPro-----GlyLysPro-----666
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QY ArgArgTrpGluProVal-----ValAspThrGlyLysProAla 720
DB CCGCACCACTGGGAGGTGTCCCGGTGTTTCAACGCAATGTGGAGCCCCCACGTCGCGG 2091
QY ProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIle 736
DB CCGCGGACAGCCTGTG-----CTCCCGCGCGCGTGTGACGCGTG 2133

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RESULT 14

US-09-252-991A-8062

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; Sequence 8062, Application US/09252991A
; Patent No.: 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8062
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8062

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Best Local Similarity: 38.69% Mismatches: 216
Query Match: 26.65% Indels: 94
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DB 103 TTCGCGCTGTCTCGGCGCCACGCGACCAAGTCGAGCTGTGCTGTTC-----GAC 153
QY 96 LeuLysAlaAspArgValThrGluValProLeuAspProLeuMetAsnAsgThrGly 115
DB 154 GCGCGCGGGAAAGGAGATCGAGCGCATCGAATGCCC-----GAGTACACCGAC 204
QY 116 AsnValTrpHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPhe 135
DB 205 GAGATCTGCGACGGCTACTCTCCGCGACGCCACACCGCGGGCGAGATCTACGCGTACCGGGTG 264
QY 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValValAsp 155
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QY 188 TyrSer-----ThrPheAspTrpGluGlyAspLeuProLeuArgTyrPro 202
DB 445 AAGTCGAAGTCATCGATCCGCGCTTCACTGGCGCGCGCGCGCGCGTACGCGTCCCC 504
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QY 223 AsnValGluHisPro-----GlyThrPheIleGlyAlaValSer 235
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QY 236 Lys-----LeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCys 253
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Job time : 6306 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2004, 03:42:31 ; Search time 1434 Seconds
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Searched: 3222919 seqs, 2451570024 residues
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Listing first 45 summaries

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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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ALIGNMENTS

RESULT 1
US-10-238-091-6
; Sequence 6, Application US/10238091
; Publication No. US20030093834A1
; GENERAL INFORMATION:
; APPLICANT: Hoechst Schering AgrEvo GmbH
; APPLICANT: LITZ, Horst
; APPLICANT: LSTTICKE, Stephanie
; APPLICANT: ABEL, Gernot
; APPLICANT: GENSCHER, Ulrich
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT
; FILE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
; FILE REFERENCE: 514413-3849.1
; CURRENT APPLICATION NUMBER: US/10/238,091
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: WO 99/58690
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: DE 198 20 608.9
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: 09/674,817
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

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3	4050	96.2	2997	15	US-10-238-091-2	Sequence 2, Appli
4	3597	85.4	2307	17	US-10-437-963-88689	Sequence 88689, A
5	3569.5	84.7	2684	13	US-10-425-114-24609	Sequence 24609, A
6	2895.5	68.7	2352	9	US-09-938-842A-218	Sequence 218, App
7	2895.5	68.7	2352	11	US-09-938-842A-218	Sequence 218, App
8	2820.5	67.0	1866	13	US-10-425-114-19788	Sequence 19788, A
9	2812	65.0	2133	10	US-09-850-936-1	Sequence 1, Appli
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13	1553.5	36.9	2729	17	US-10-437-963-39232	Sequence 39232, A
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17	1305.5	31.0	1995	13	US-10-282-122A-18612	Sequence 18612, A
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19	1300	30.9	1998	9	US-09-841-132-430	Sequence 430, App
20	1294.5	30.7	2103	16	US-10-369-493-42960	Sequence 42960, A
21	1283.5	30.5	2106	16	US-10-369-493-43657	Sequence 43657, A
22	1268	30.1	2163	16	US-10-369-493-47096	Sequence 47096, A
23	1264	30.0	2001	13	US-10-282-122A-18954	Sequence 18954, A
24	1261	29.9	2039	16	US-10-369-493-34873	Sequence 34873, A
25	1239.5	25.4	2103	16	US-10-369-493-33678	Sequence 33678, A
26	1225.5	25.1	2256646	17	US-10-470-565-1	Sequence 1, Appli
27	1221.5	25.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
28	1211	28.8	2037	16	US-10-369-493-39257	Sequence 39257, A
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30	1206	28.6	2031	16	US-10-369-493-39630	Sequence 39630, A
31	1204	28.6	2508	9	US-09-738-626-2305	Sequence 2305, Ap
32	1204	28.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
33	1203.5	28.6	2106	16	US-10-156-761-2139	Sequence 2139, Ap
34	1192.5	28.3	2082	16	US-10-369-493-39143	Sequence 39143, A
35	1187.5	28.2	2082	16	US-10-369-493-39890	Sequence 39890, A
36	1187.5	28.2	2115	16	US-10-369-493-39511	Sequence 39511, A
37	1187	28.2	2181	9	US-09-833-435A-12	Sequence 12, Appl
38	1187	28.2	2181	15	US-10-375-720-12	Sequence 12, Appl
39	1186.5	28.2	2247	15	US-10-156-761-2776	Sequence 2776, Ap
40	1183.5	28.1	2226	16	US-10-369-493-28419	Sequence 28419, A
41	1179	28.0	2082	16	US-10-369-493-32052	Sequence 32052, A
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RESULT 2

US-10-238-091-1
; Sequence 1, Application US/10238091
; Publication No. US20030093834A1
; GENERAL INFORMATION:
; APPLICANT: Hoechst Schering AgrEvo GmbH
; APPLICANT: LTRZ, Horst
; APPLICANT: LSTTICKS, Stephanie
; APPLICANT: ABEL, Gernot
; APPLICANT: GENSCHER, Ulrich
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT
; FILE REFERENCE: 514413-3849.1
; CURRENT APPLICATION NUMBER: US/10/238,091
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: WO 99/58690
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: DE 198 20 608.9
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: 09/574,817
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Triticum aestivum L. cv.Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(296)
; OTHER INFORMATION:
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; LOCATION: (397)..(1617)
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US-10-238-091-1

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Qy 1 SerGlyProAlaProArgLeuArgArgTrpArgProAsnAlaThrAlaGlyLysGlyVal 20
Db 3 TCGGGGCGCGCGCGCGCTCGACGCGTGGCGACCCCAATCGCGGGGAAAGGGGTC 62
Qy 21 GlyGluValCysAlaAlaValValGluAlaThrLysValGluAspGluGlyGluGlu 40
Db 53 GCGAGGTGTGCGCGCGGTTCGAGCGCGCGACGAGGTAGAGACGAGGGGAGAG 122
Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGly 60
Db 123 GACGAGCGGTGGCGGAGGACAGTACGCTCGCGCGCGCTGACAGGGTCTCGCGGA 182
Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80
Db 183 ATGCCCGCGCGTGGCGCGCACCGCGCTCGCGCGCGGTCAATTTGCGCGTCTATTCC 242
Qy 81 GlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97
Db 243 GCGGAGCCACCGCGCGCGCTCTGCTCTTCAGGCCAGAGATCTCAAGGCGGTGGGG 302
Qy 97 ----- 97
Db 303 TTGCTCCCGAGTAGAGTTTCATCAGCTTTCGCGCGCGCGCTTTTGGGCGCTG 362
Qy 98 -----Ala-AspArgValThrGluGluValProLe 107
Db 363 CAATTAAAGTTTGTACTGGGCAATGCTGACGATAGGCTACCGAGAGAGTTCCTCCT 422
Qy 107 uAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyLeuHi 127
Db 423 TGACCCCTGATGAATCGGACCGGCAACGTTGCGCATGTCTTCATCGAAGCGAGTGA 482
Qy 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe 147
Db 483 CAACATGCTTTACGGGTACAGGTTGACGGCACCTTTGCTCTCTCACTGCGGCACTACCT 542
Qy 147 uAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTy 167
Db 543 TGATGTTTCCAAATGCTGCTGCTGATCTTATGCTAAGCAGTGATTAAGCCGAGGGAGTA 602
Qy 167 xGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPr 187
Db 603 TGGTGTTCACGCGCGTGGTAACAAATGCTGCGCTCAGATGGCTGGCATGATCCCTCTTC 662
Qy 187 oTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuVa 207
Db 663 ATATAGCACGTTTGATGGAGCGCGACCTACCTCTAAGATATCTCAAAAGACCTGGT 722
Qy 207 lIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227
Db 723 AATATATGAGATGCACTTGGTGATTCAGAGCATGATTCAAGCAATCTAGAACATCC 782
Qy 227 oGlyThrPheIleGlyValaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCy 247
Db 783 GGGTACTTTCATTGGAGCTGTGTGCGAGCTTGACTATTTGAAGAGAGCTGGAGTTAATTG 842
Qy 247 sIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSerLy 267
Db 843 TATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCAA 902
Qy 267 sMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSe 287
Db 903 GATGAACCTTTGGGGATATTCTACCAATAACTTCTTTTCCCAATACCAAGATACACATC 962
Qy 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGl 307

Db 963 AGCGGGATAAAAAAGTGGGGGATGATGCCATAAATAGTTCACAACTTTTGTAAAGGA 1022
QY 307 uAlaHisArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGl 327
Db 1023 GGCTCACAACGGGAATAGGTGATCCTGGATGTTCTTCAACCATACAGCTGAGGG 1082
QY 327 yAsnGluAsnGlyProIleLeuSerPheIysGlyValAspAsnThrThrTyMetLe 347
Db 1083 TAATGAGAATGTCGAATATATCAATTAAGGGGTCCGTAATCTACTATATATGCT 1142
QY 347 uAlaProIysGlyGluPheTyAsnTySerGlyCysGlyAsnThrPheAsnCysAsnHi 367
Db 1143 TGCACCCAGGAGAGTTTATAACTATCTGGCTGTGGGAATACCTTCAACTGTGAATCA 1202
QY 367 sProValValArgGlnPheIleValAspCysLeuArgTyTrpValThrGluMetHisVa 387
Db 1203 TCGTGTGGTTCGTCATTCATTTAGATGTTTAAAGATACCTGGGTGACGGAATGCATGT 1262
QY 387 lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspPr 407
Db 1263 TGATGCTTTTCTGTTGATCTTCATCCATATGACAGAGGTCCAGTCTGTGGATCC 1322
QY 407 oValAsnValTyGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuVa 427
Db 1323 AGTTAACGTGTATGAGCTCCCAATAGAAGTGACATGATCAACACAGGGACACCTCTTGT 1382
QY 427 lThrProProLeuIleAspMetIleSerAsnAspProIleLeuGlyValLysLeuIl 447
Db 1383 TACTCCACCATATATGACATGATCAGCAATGACCAATCTTGGAGCGTCAGCTCAT 1442
QY 447 eAlaGluAlaTrpAspAlaGlyGlyLeuTyrglnValGlyGlnPheProHisTrpAsnVa 467
Db 1443 TCGTGAAGCATGGGATGACAGGAGCTCTATCAAGTAGTCAATTCCTCACTGCGAATGT 1502
QY 467 lTrpSerGluTrpAsnGlyIysTyArgAspIleValArgGlnPheIleLysGlyThrAs 487
Db 1503 TTGGTCTGAGTGGGAATGCGGAGATACCGGACATTTGGCTCAATTCATTAAGGCACTGA 1562
QY 487 pGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrglnAla-- 506
Db 1563 TGAATTTGCTGGTGGTTTGGCGAATGCTTTGTGGAGTCCACACCTATACCAGGT-AA 1621
QY 506 ----- 506
Db 1622 GTTGTGGCAATATCTGTAAATGAGTTGAGTGAATGTCACTGGATTTTATATATACCA 1681
QY 506 ----- 506
Db 1682 CATGATGATACATCTAAATATATAAATCATAGTGTATGCATATGCATTTGGCTAAG 1741
QY 506 ----- 506
Db 1742 AAGTATTAGTGATACACTAGTGTATATATAGTTTAAACCCCACTTGCCAATGAAG 1801
QY 506 ----- 506
Db 1802 GAACATAGGCGTTTCTAGTTATCTTATTTATTTGTCGGTGAATATCCACTGAATAAAT 1861
QY 506 ----- 506
Db 1862 CCAGCCATGTCTATTTTATAGGGGGGAGAAAGAACTATATTGATTTGGCCCCCTAAAGA 1921
QY 506 ----- 506
Db 1922 AGCCATCTCAGAAATCATAGTAAGTTGCTTTTCTGTAAAGAAAGAAAGAAAGCTTCATA 1981
QY 506 ----- 506
Db 1982 CTTTCTACGGTGCTAACTAGCTCGATGATATTTGTAAGATGAATGCCAAATTAAT 2041
QY 506 ----- 506

Db 2042 TGTCGGATAATTGATCTGTATTACAAATTTCTATTGGTTTCTTAGAATCAAAACC 2101
QY 507 ----- GlyIysArgLysPr 511
Db 2102 AGTAACCTGTTATTGGCACTGCACTTCTTATTGATTATTAATCAGGAGGAGGAGAAACC 2161
QY 511 oTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTh 531
Db 2162 TTGGCAGACATCACTTTGTATGTCACATGATGATTTACACTGGCTGATTTGTTAAAC 2221
QY 531 rTyAsnLysLysTyAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAs 551
Db 2222 ATATAATAAGAGATCAATTTTACCAATGGGAGAACAAACAGAGATGGAGAAATACAA 2281
QY 551 nLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValIysArgLeuAr 571
Db 2282 TCTTAGCTGGAATTTGGGGAGGAGAGAAATTCGCAAGATTTCTGTCAAAAGATTGAG 2341
QY 571 gLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPh 591
Db 2342 GAAGAGGCGAGATCGCAATTTCTTTTGTCTCATGGTTTCTCAAGGAGTTCCAAATGT 2401
QY 591 eTyMetGlyAspGluTyrglyHisThrLysGlyGlyAsnAsnAsnThrTyCysHisAs 611
Db 2402 CTACATGGGTGATGAATATGGCCACAAAGGGGCAACACATACATACATATGCCATGA 2461
QY 611 pSerTyValAsnTyPheArgTrpAspLysLysGluGlnTyrglnTySerGluLeuHisArgPh 631
Db 2462 TTCTTATGTCAATTTTTCGCTGGGATATAAAGAAACAAATACTCTGAGTTGACCGATT 2521
QY 631 eCysCysLeuMetThrLysPheArgLysGluCysGlyGlyLeuGlyLeuGluAspPhePr 651
Db 2522 CTCTCGCTCATACCAATTTCCGAAGGAGTCCGAGGGTCTTGGCCTTTGAGACCTTTC 2581
QY 651 oThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAs 671
Db 2582 AACGGCCAAACGCTGCTGAGTGGCATGTCATCAGCTGGGAGGCTGATTGGTCTGAGAA 2641
QY 671 nSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyValAlaPh 691
Db 2642 TAGCCGATTTCTGCTCTTTTCCATGAAGATGAACACAGGCGGAGATCTATGTGCGCTT 2701
QY 691 eAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgArgTrpGl 711
Db 2702 CAACACGACCATTTACCGCGCTTGTGAGTCTCCAGAGCGCGCGCGGTGGGA 2761
QY 711 uProValValAspThrGlyLysProAlaProTyArgPheLeuThrAspLeuProAs 731
Db 2762 ACCGGTGTGGACACAGGCAAGCCAGCACCATACGACTTCTCCACGCGAGCTTACCTGA 2821
QY 731 pArgAlaLeuThrIleHisGlnPheSerHisPheLeuTySerAsnLeuTyProMetLe 751
Db 2822 TCGCGCTCTCACCATACACAGTTCTCGCATTTCTCTACTCCAACTCTACCCCATGCT 2881
QY 751 uSerTySerSerValIleLeuValLeuArgProAspVal 764
Db 2882 CAGCTACTCATCGTCTATCTAGTATTGGCCCTGATGTT 2921

RESULT 3

US-10-238-091-2

; Sequence 2, Application US/10238091

; Publication No. US20030093834A1

; GENERAL INFORMATION:

; APPLICANT: Hoechst Schering AgrEvo GmbH

; APPLICANT: LFEZ, Horst

; APPLICANT: LSTTICKE, Stephanie

; APPLICANT: ABEL, Gernot

; APPLICANT: GENSCHKE, Ulrich

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT

; TITLE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH

; FILE REFERENCE: 514413-3849.1

; CURRENT APPLICATION NUMBER: US/10/238,091

; CURRENT FILING DATE: 2002-09-10

; PRIOR APPLICATION NUMBER: WO 99/58690
 ; PRIOR FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: DE 198 20 608.9
 ; PRIOR FILING DATE: 1998-05-08
 ; PRIOR APPLICATION NUMBER: 09/674,817
 ; PRIOR FILING DATE: 2000-11-06
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 2997
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum L. cvFlorida
 US-10-238-091-2

Alignment Scores:

Pred. No.: 0 Length: 2997
 Score: 4050.00 Matches: 763
 Percent Similarity: 78.34% Conservative: 0
 Best Local Similarity: 78.34% Mismatches: 1
 Query Match: 96.15% Indels: 211
 DB: 15 Gaps: 2

US-09-674-817B-3 (1-764) x US-10-238-091-2 (1-2997)

QY 1 SerGlyProAlaProArgLeuArgArgTyrArgProAsnAlaThrAlaGlyLysGlyVal 20
 Db 3 TCGGGCCGCGCGCGCGCTGGAGCGTGGCGACCCCAATGCGACGCGCGGGAGGGGTC 62
 QY 21 GlyGluValCysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlu 40
 Db 63 GCGAGGTGTGCGCGCGCGTGTGCGAGCGCGCGCGAGGAGTAGAGGACGAGGGGAGGAG 122
 QY 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyValaCysArgValLeuAlaGly 60
 Db 123 GACGACCGGTGGCGAGGACAGGTACGCGCTCGCGCGCGCGTGGCGGTGTCTCCCGGA 182
 QY 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValaAspPheAlaValTyrSer 80
 Db 183 ATGCCCGCGCGCTGGCGCGCGCGCGCTGGCGCGCGCGGTCAAATTCGCGCTCTATTCC 242
 QY 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97
 Db 243 GCGGAGACCCCGCGCGCGCTGTGCTCTTCACGCCAGAGACTCAAGCGCGGTGGG 302
 QY 97 ----- 97
 Db 303 TTGCTCCCGAGTAGAGTTTCATCAGCTTTGCGTGGCGCGCGCGCTTTTGGGCGCTG 362
 QY 98 -----Ala-AspArgValThrGluGluValProle 107
 Db 363 CAATTAAAGTTTGTACTGGGGCAATGCTGCAGGATAGGGTGACCGAGGAGTTCCCT 422
 QY 107 uAspProLeuMetAsnArgThrGlyAsnValTyrHisValPheIleGluGlyGluLeuHi 127
 Db 423 TGACCCCTGATGAATCGACCGGNACTGTGGCATGTCTTCATCGAAGGCGAGCTGCA 482
 QY 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrIle 147
 Db 483 CAACATGCTTACGGGTACAGGTTCGACGCGACCTTTGCTCTCACTGCGGCGACTACT 542
 QY 147 uAspValSerAsnValValaAspProTyrAlaLysAlaValIleSerArgGlyGluTy 167
 Db 543 TGAATTTTCATGCTGCTGGTATCTTATCTAGGCGAGTGAAGCCGAGGGAGTA 602
 QY 167 rGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAlaGlyMetIleProLeuPr 187
 Db 603 TGTGTATCCAGCGCGTGTAAACAATGTCTGGCTCAGATGGCTGGCATGATCCCTCTCC 662
 QY 187 oTyrSerThrPheAspTyrGluCysLeuProLeuArgTyrProGlnLysAspLeuVa 207
 Db 663 ATATAGCAGGTGTGATTGGGAAGGGGACCTACTCTTAAGATATCTCAAAAGGACCTGTT 722
 QY 207 lileTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227

Db 723 AATATATGAGATGCACCTTGGGTGATTACAGAACATGATTCAAGCAATGTAGAACATCC 782
 QY 227 cGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCy 247
 Db 783 GGGTACITTCATTTGGAGCTGTGTCGAAGCTTGACTATTGAAGGAGCTTGGAGTAATTG 842
 QY 247 sileGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerLy 267
 Db 843 TATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGAGTACTCAACCTCTTCTTCCAA 902
 QY 267 sMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSe 287
 Db 903 GATGAACITTTGGGATATTCTACCATTAACCTCTTTTCCCAATGACAGATACACATC 962
 QY 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgG 307
 Db 963 AGCGGGATAAAAAAGCTGTGGCGTGTGATGTCATAAATGAGTTCAAACTTTTGTAGAGA 1022
 QY 307 uAlaHisIysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluG 327
 Db 1023 GGCACAAACGGGGAATTGAGGTGATCCTGGATGTTGCTTCAACCATCAGCTGAGGG 1082
 QY 327 yAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLe 347
 Db 1083 TAATGAGAAATGGTCCAATATTATCATTTAAGGGGTGCGATAATACTACATATATGCT 1142
 QY 347 uAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHi 367
 Db 1143 TGCACCAAGGAGAGATTTATATACTATTCTGGCTGTGGGAATACCTTCAACTGTAATCA 1202
 QY 367 sProValValArgGlnPheIleValAspCysLeuArgTyrTyrValThrGluMetHisVa 387
 Db 1203 TCCTGTGTTTGGTTCATTTAGATGTTTAAAGATCTGGGTGACGGAATGCAATG 1262
 QY 387 lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspPr 407
 Db 1263 TGATGGTTTTCGTTTGTATCTTGCATCCATAATGACGAGGTTCCAGTCTGTGGGATCC 1322
 QY 407 oValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuVa 427
 Db 1323 AGTTAAGGTATGAGCTCCATAGAAGGTGATGATCACAACAGGACACCTCTTGT 1382
 QY 427 lThrProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuI 447
 Db 1383 TACTCCACCACTTATTGACATGATCAGCAATGACCAATTTCTTGGAGCGCTCAAGCTCAT 1442
 QY 447 eAlaGluAlaTyrAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTyrAsnVa 467
 Db 1443 TGCTGAAGCATGGGATGACGAGGCGCTTATCAAGTAGGTCAATTCCTCCTCAGTGAATGT 1502
 QY 467 lTyrSerGluTyrAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAs 487
 Db 1503 TTGCTCTGAGTGGAAATGGGAAGTACCGGACATTTGCGTCAATTCATTAAAGGCACTGA 1562
 QY 487 pGlyPheAlaGlyCysLeuGluCysLeuCysGlySerProHisLeuTyrGlnAla-- 506
 Db 1563 TGGATTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1621
 QY 506 ----- 506
 Db 1622 GTTGTGCAATCTTGTAAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATACCA 1681
 QY 506 ----- 506
 Db 1682 CATGATGATACACATCTAAATATATAACAATCATAGTGTATGCATATGCTATTTGGCTAAG 1741
 QY 506 ----- 506
 Db 1742 AAGTATTAGTATACACTAGTGTATATATAGTTTTAAACCCCACTTGGCAATGAAG 1801
 QY 506 ----- 506

Db 1802 GAACATAGGGCTTTCTAGTATCTTATTATTGTCGGTGAATAATCCACTGAAAAATT 1861
QY 506 ----- 506
Db 1862 CCAGCCATGTCATTTTTTAGGGGGGAGNAGAACTATATTGATTTGCCCCCTTAAAGA 1921
QY 506 ----- 506
Db 1922 AGCCATCTCAGAATTCATAGTAAGTGTCTTTCTGTAAAGAAAGAAAGAGCTTCATA 1981
QY 506 ----- 506
Db 1982 CTTTCTATCGGTGCTAACTTAGCTCGATGATATATTGTGAAGATGCAAAATTTAATT 2041
QY 506 ----- 506
Db 2042 TGTCCGATAATTGATCTGTATTACAAATTTCTATTGTTTCTAGAAATCAAAACC 2101
QY 507 ----- GlyGlyArgLysPr 511
Db 2102 AGTAACCTGTTATTGSCACTGCAACTTCTATTGATTAAATCAGGCAGGAGGAAGAAACC 2161
QY 511 oTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTh 531
Db 2162 TTGGCACATATCAACTTTGTATGTGCATATGATTTACACTGGCTGATTTGGTAAC 2221
QY 531 rTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAs 551
Db 2222 ATATAATAAGAGTACAAATTTACCAATGGGAGAACCAACAGAGATGGAGAAATACAA 2281
QY 551 nLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuAr 571
Db 2282 TCTTAGCTGCAATTTGGGGAGAGAGAAATTCAGAAATTTCTCTCAAAAGATTGAG 2341
QY 571 gLysArgGlnMetArgAsnPheValCysLeuMetValSerGlnGlyValProMetPh 591
Db 2342 GAAGAGCAGATGCGCAATTTCTTTGTTGTTCTCATGTTTCTCAAGGAGTTCCAATGTT 2401
QY 591 eTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAs 611
Db 2402 CTACATGGGTGATGAATATGGCCACACAAAGGGGGCAACACAAATACATATCGCATGA 2461
QY 611 pSerTyrValAsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPh 631
Db 2462 TTCATTATGTCATTTTCGTGGATPAAAGAAAGACAAATCTCTGATTTGCACCGATT 2521
QY 631 eCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPhePr 651
Db 2522 CTGCTGCCTCATGACCAAAATTCGCAAGGAGTGCAGGGTCTTGGCCTTGAGGACTTTCC 2581
QY 651 oThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAs 671
Db 2582 AACGGCAAAACGGTGCAGTGCATGGTTCATCAGCTCGGAAGCTGATTTGGTCTGAGAA 2641
QY 671 nSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPh 691
Db 2642 TAGCCGATTCGTTGCTTTTCCATGAAGATGAAAGACAGGGCGAGATCTATGTGGCCTT 2701
QY 691 eAsnThrSerHisLeuProAlaValGluLeuProGluArgAlaGlyArgArgTrpGlu 711
Db 2702 CAACACACGCCACTTACCGGGCGTGTGTAGCTCCAGAGCGCGAGGGCGCGGTGGGA 2761
QY 711 uProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAs 731
Db 2762 ACCGGTGGTGGACACAGCAAGCCAGCACATACGACTTCTCTACCGAGCATTTACCTGA 2821
QY 731 pArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLe 751
Db 2822 TCGCGCTCTCAACATACACAGTTCTCGCATTTCTCTACTCCAACTCTACCCCATGCT 2881
QY 751 uSerTyrSerSerValIleLeuValLeuArgProAspVal 764
Db 2882 CAGCTACTCATCGGTCACTCTAGTATTGGCCCTCTGATGTT 2921

RESULT 4

US-10-437-963-88689
; Sequence 88689, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88689
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MPT4530_87515C.1
US-10-437-963-88689

Alignment Scores:
Pred. No.: 0 Length: 2307
Score: 3597.00 Matches: 644
Percent Similarity: 92.98% Conservative: 31
Best Local Similarity: 88.71% Mismatches: 45
Query Match: 85.40% Indels: 6
DB: 17 Gaps: 1

US-09-674-817B-3 (1-764) x US-10-437-963-88689 (1-2307)

QY 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAla 63
Db 13 GTGATCGGAGAGGTACCGCTGGGTGGCGCTGCAGGGTCTCCCGGATGCCCG 72
QY 64 ProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGlyGlyAla 93
Db 73 CCGCTCGGGGCCACCGCTCGACGGCGGGTCAATTCCCGCTCTACTCCGCGCGCA 132
QY 84 ThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgValThrGlu 103
Db 133 TCCGCGCGCGTCTGCTCTTCACCCCGACGATCTCGAGCGGATGAGGTGACTGAG 192
QY 104 GluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGlu 123
Db 193 GAGGTTCCGCTTGATCTCTGTTCAATCGGACGGGGAATGTGTGGCACGCTTCATCGAA 252
QY 124 GlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCys 143
Db 253 GGGCAGCTGCACAAATGCTGTACGGGTACAGGTTCCGATGGTATGTTCCCGCTCACTGC 312
QY 144 GlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaValIleSer 163
Db 313 GGCAGTACTTCGATGTCTCCAAATGTCGTGGTGGATCTTATGCCAAGGAGGTGATAAGC 372
QY 164 ArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMet 183
Db 373 CGAGGAGATGATGGTGTCCCGGTCTCTGTGTGGGATTTGTGGCCTCAATGGCTGCATG 432
QY 184 IleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGln 203
Db 433 ATCCCTCTCCGTACAGTACGTTTGAATGGCAAGGTGACCTACCTCTGAGATATCTCAG 492
QY 204 LysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsn 223
Db 493 AAGGATCTTGTAAATCTATGAGATGCAATTTACGTGGGTTTACAAAGCACAGTTCAGCAAT 552

QY 224 ValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeu 243
 Db 553 GTAGAACATCCAGGACTTACATGGGGCTATATCAAGCTTGACATCTCGAAGAGCTT 612
 QY 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263
 Db 613 GGAGTTAACTGTGTAGAGTTGATGCCCTCGCCATGAATTCAAATGAGCTGAGTACTTCAGC 672
 QY 264 SerSerSerLysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThr 283
 Db 673 TGTCTCTCCAGATGAACCTTCGGGGATCTCCACGATAAACTTTTTCACCAATGATA 732
 QY 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
 Db 733 AGATATTATCATAGTGGGATAAGAACTGTGGCCGTGATGCCATAAATGAATTCAAAAC 792
 QY 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValPheAsnHis 323
 Db 793 TTGTGTAGAGAGCTCACAAACGGGAATGAGGTGATCATGGATGTTGTCTTCAATCAT 852
 QY 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343
 Db 853 ACAGCCGAGGTAATGAGAAAGGACCAATATTATCATTTAGGGGATAGATAATAGCACA 912
 QY 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
 Db 913 TACTATATGCTGCCCTAAGGAGAGATTTTACAATATTCTGGTGTGGGAATACCTTC 972
 QY 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThr 383
 Db 973 AACTGTAAATCATCTCTGTCGTCGTGAATTTATGTAGATTGTTAAGATCTGGTGACA 1032
 QY 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
 Db 1033 GAAATGCATGTTGATGGTTTTCGTTTGTATCTTGCATCCATATGACCAGAGGATGCCAGT 1092
 QY 404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423
 Db 1093 CTTTGGGATCCAGTTAATGTGTATGGAGTCCAGTAGAAGGTGACATGATACGACAGGG 1152
 QY 424 ThrProLeuValThrProProLeuLeuAspMetIleSerAsnAspProIleLeuGlyGly 443
 Db 1153 ACACCTCTTGTCTACTCCACCCTATTATGACATGATCAGCAATGATCCAAATCTTCGAGAT 1212
 QY 444 ValLysLeuIleAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463
 Db 1213 GTCAAGCTCATGCTGAAGCATGGGATCGGGAGGCTCTATCAAGTAGTCAATTTCTCT 1272
 QY 464 HisTrpAsnValTrpSerGluTrpAsn-----GlyLysTyrArgAsp 477
 Db 1273 CACTGGAAAATTTGGTCAGATGGAATGGAAGGGCATGGGTTATGGAAGTACCGGAC 1332
 QY 478 IleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeu 497
 Db 1333 AVTGTTCGTCAATTCATTAAAGGCACAGATGGATTTCGTGTGGTTTCGCTGAAATGTTG 1392
 QY 498 CysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPhe 517
 Db 1393 TGTGGAGTCCCACTATACCGAGCGGGGGAGGAACCTTGGCAGATATCAACTTT 1452
 QY 518 ValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsn 537
 Db 1453 GTGTGTGCGCATGATGGATTTACGCTGCTGATTTGGTGACATATAACAAGAAGTACAAC 1512
 QY 538 LeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGly 557
 Db 1513 TCTTCAAAATGGTGAGATTAATAGATGGAGAAATCATCACTCAGCTGGAACTGTGGG 1572
 QY 558 GluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsn 577
 Db 1573 GAGGAAGGAGAAATTCACGGTTTGTCTCGTCAAAAGATTGAGGAGGCAATGCGCAT 1632

QY 578 PhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyr 597
 Db 1633 TTCTTTGTTTCTCTCATGGTTTCTCAAGGTGTTCCGATGTTCTACATGGGCGATGATAT 1692
 QY 598 GlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPhe 617
 Db 1693 GGCCATACAAAGAGGACCAACAACACATCTACTGCCCATGACCAATTATGTCAATTATTTC 1752
 QY 618 ArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLys 637
 Db 1753 CGCTGGGACAAAGAAGAAATCCTCTGACTTGCACCGTTCTGCTCTCTTATGACCAAA 1812
 QY 638 PheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGln 657
 Db 1813 TTCCGCCAAACAATCGGAGTCCCTTGGCTCGCAGACTTCCCAACAGCTCAACGGTTGCAT 1872
 QY 658 TrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPhe 677
 Db 1873 TGGCATGCCATACGCTTGGAAACCTGACTGGTCTGAGACAAGCCGTTTTCGTGGCCCTTC 1932
 QY 678 SerMetLysAspGluArgGlnGlyIleTyrValAlaPheAsnThrSerHisLeuPro 697
 Db 1933 TCCACGAAGATGAACGAAGGCGAGATCTACGTGGCTTCAACGCCAGCAATTTGCCG 1992
 QY 698 AlaValValGluLeuProGluArgAlaGlyArgArgTrpGluProValValAspThrGly 717
 Db 1993 GCGTTGTGTGACTCCACAGAGCCCGCTACCGCTGGAGCGGCTGGTGGACACAGGC 2052
 QY 718 LysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHis 737
 Db 2053 AAGCAGCGCTTATGACTTCTCCACGACGACCTGCTGATCGTGTCTACGCGGTCCAC 2112
 QY 738 GlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValle 757
 Db 2113 CTGTCTCTCTATTTCTTCAATCCAAATCTTACCCATGCTCAGCTACTCTCCTCATC 2172
 QY 758 LeuValLeuArgProAsp 763
 Db 2173 CTTGAATGGACGCTGAT 2190

RESULT 5

US-10-425-114-24609
 ; Sequence 24609, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 24609
 ; LENGTH: 2684
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3632-046-B8_FLI
 US-10-425-114-24609

Alignment Scores:
 Pred. No.: 0 Length: 2684
 Score: 3569.50 Matches: 653
 Percent Similarity: 90.28% Conservative: 44
 Best Local Similarity: 84.59% Mismatches: 65
 Query Match: 84.75% Indels: 10
 Gaps: 4

US-09-674-817B-3 (1-764) x US-10-425-1114-24609 (1-2684)

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QY 2 GlyProAlaProArgLeuArg-ArgTyrArgProAsnAlaThrAlaGlyLysGlyValGI 21
Db 175 GGGCCGGTGGCGCGGGCGTGGCGGGCGGCCCAAT---GTGGCGGACTGGGGCGGGG 231
QY 21 yGluVal-----CysAlaAlaValValGluAlaAlaThrLysValGI 35
Db 232 GCGGCTGTCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGGA 291
QY 35 uAspGluGlyGluGluAspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCy 55
Db 292 GGACGACGACGACGACGACGAGAGTGGCCGAGAGAGTTCGGCTGGGGCGCGCGGTG 351
QY 55 sArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyLysValAs 75
Db 352 CCGGGTGTCTCGCGGAAATCCCGCGCGCTCGCGGCCACCGCGCTCCGCGCGGTGTCAA 411
QY 75 nPheAlaValTyrSerGlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAs 95
Db 412 CTTGCGCGGTCTACTCCAGCGGTGCTCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 471
QY 95 pLeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGI 115
Db 472 CCTCAAGCGGATAGGTGACCGGAGAGGTGCCCTCGATCCCTGCTCAACCGAACGGG 531
QY 115 yAsnValTyrHisValPheIleGluGly---GluLeuHisAsnMetLeuTyrGlyTyrAr 134
Db 532 AAACGTGTGGCAGTGTTCATCCAGCGGACAGCTGCACGCGCATGCTCTACGGATACAG 591
QY 134 gPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValVa 154
Db 592 GTTCGATGGCGTGTTCGCGCCCTGACGCGGACAGTACTACGATGTCCACGTTGTGCT 651
QY 154 lAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAs 174
Db 652 GGATCCATACGTCATAGCGAGTGTAAAGCGAGTGAATATGTTGTCCTGCGCGCTGTTGG 711
QY 174 nAsnCysTyrProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTyrGI 194
Db 712 TAGTTTGTGGCTCAAAATGGCTGGTATGATTCCTCTTCCCTATAAATGATTGATGCA 771
QY 194 uGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuAr 214
Db 772 AGGTGACCTACCCCTTGGGTACCATCAGAAGACCTTGTATATATGAATGCAATTTGCG 831
QY 214 gGlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVa 234
Db 832 TGGATTTCACAAAGCACAACTCAAGCAAGACAAACACCCAGGAACCTTACATTGGTGTGT 891
QY 234 lSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHi 254
Db 892 GTCAAGCTTGACCATCTAAGGAACCTTGGAGTGAACCTGTATAGAGTAAATGCCCTGCCA 951
QY 254 sGluPheAsnGluLeuGluTyrSerThrSerSerSerLysMetAsnPheTyrGlyTyrSe 274
Db 952 TGAGTTCAATAGCTAGTACTTACGCTCCTCTTCGAGATGAACCTTCGCGGGATATTC 1011
QY 274 rThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGI 294
Db 1012 CACAAATAATTTTCTCCACCAATGGCAAGATATTTCTTCAGTGGCATAAGAGACTCTGG 1071
QY 294 yArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGI 314
Db 1072 ATGTGTCGCATAAATGAATTTAAAGCTTTTGTAAAGGAGGCGCCACAAACGGGGAATTGA 1131
QY 314 uValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLe 334
Db 1132 GGTGATCATGGATGTTGTCTTCAATCATACACTGAGGTAAATGAGAAAGGCCCAATATT 1191
QY 334 uSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr 354
Db 1192 ATCCTTTAGGGGATAGATAATAGTACTACTACATGCTTGCACCTTAAGGGAGAGTTTA 1251
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QY 713 lValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAl 733
Db 2332 GGTGGACACGGCAAGGAGCACCATATGACTTCTCCACCGATGGCCGACAGATCGTGC 2391
QY 733 aLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTy 753
Db 2392 TGTACCGGCTACCGAGTCTCTCATTTCTCACTCAATCTATCTATCTATCTATCTATCT 2451
QY 753 rSerSerValIleLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 764
Db 2452 CTCCTCCATCATCTCTGTATTGGCCCTGATGTC 2485

RESULT 6

US-09-938-842A-218
; Sequence 218, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 218
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-218

Alignment Scores:

Pred. No.: 0 Length: 2352
Score: 2895.50 Matches: 518
Percent Similarity: 81.08% Conservative: 82
Best Local Similarity: 70.00% Mismatches: 127
Query Match: 68.74% Indels: 14
DB: 9 Gaps: 4

US-09-674-817B-3 (1-764) x US-09-938-842A-218 (1-2352)

QY 29 GluAlaAlaThrLysValGluAspGluGlyGluGluAspGluProValAlaGluAspArg 48
Db 140 GAAGAAGCAACGAAGCT-GAAATATCGCCGTAGTAGAGAAACCTCTTAAATCAGATAGA 198
QY 49 TyrAlaLeuGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68
Db 199 TTTTATCTCCGAT-----GGACTTCTCTCCATTCCGACCCACC 240
QY 69 AlaLeuAlaGlyLysValAsnPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeu 88
Db 241 GTCAGAGACGACGGCGTCAATTTCTGTGTACTTACAACTCCGTTTCGCTACCATC 300
QY 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108
Db 301 TCTTGATTTCTCTCCGATCTCCGTGAGAACAAAGTGACGAGGAGGATTCAGCTTGAT 360
QY 109 ProLeuMetAsnArgThrGlyAsnValTrpPheIleGluGlyGluLeuHisAsn 128
Db 361 CCATCAAGGATAGAACTGGCCATGTTGGCATGTGTTCTTGAGAGGAGATTCAGAGAT 420
QY 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
Db 421 ATGTTGTATGTTATAGATTGATGGCAAGTTTCTCTCTGGAAGGATTCATTTATGAT 480

QY 149 ValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGly 168
Db 481 TCCITCCACATTTATTGGATCTTACCAAGCAATTAAGCAGAGATGAGTTGGA 540
QY 169 ValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyr 188
Db 541 GTTTGGGACCTGATGATAAATTGTTGGCTCAAAATGGCTGTATGGTACCCACCTCGTAG 600
QY 189 SerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
Db 601 GAAGAGTTTGATTGGGAAGGGATATGCACTGAGCTTCCACAGAAAGATCTTGTATA 660
QY 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
Db 661 TATGAATGCAATGTCGAGGTTTACCAAGGCATGAGTCTAGTAAATTAATTCCTCGGC 720
QY 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248
Db 721 ACATACAGGGTGTGACAGAGAGCTTGACCAITTGAGGAGCTTGGGATAAATTGTATA 780
QY 249 GluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSer----- 266
Db 781 GAATTAATGCCATGTCACGAGTTTAAATGAGCTGAGTATTACAGCTACAATACGATTTG 840
QY 267 -----LysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 841 GGAGACCACAGGGTAAATTTTGGGGTACTCTACCAATTCGGTCTTCTCGCCCATGATC 900
QY 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
Db 901 AGATACGCATCAGCAAGCTCTAACAATTTGCTGGACGACCCATAAATGAATTCAAAATT 960
QY 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHis 323
Db 961 CTTGTTAAGGAGGCACATAAAGAGAAATGAGGTAATCATGATGTCGCTTGAACAC 1020
QY 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343
Db 1021 ACAGCCGAGGGAATGAAAAGGGCCCATTTTCTATTAGAGAGTTGATAACAGTGC 1080
QY 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
Db 1081 TATTACATGCTGCTCCAAAGGCGAGTTCTATAATATTATTCAGGCTGTGTAATACATTC 1140
QY 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThr 383
Db 1141 AACTGCAATCATCTGTTGGTGCCTCAATTCATATGATTCGATTCGCTGAGATATCGGTACA 1200
QY 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
Db 1201 GAAATGCATCTTGACGGCTCCGCTTTGATCTTGGTTCATCATCATGTCAGGACGACGAGC 1260
QY 404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423
Db 1261 CTTTGGGATGACGCCAATGTTTACGGGGCTGATGTAGAAGGTGACTTGTCTCACAACCTGGT 1320
QY 424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGly 443
Db 1321 ACTCTTATTAGCTGCCCTCCAGTAATGACATGATGATGATGATGATGATGATGATGATG 1380
QY 444 ValIleLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPhePro 463
Db 1381 GTTAAAGCTAATAGCTGAAGCATGGGATGGGGTGGGCTGTACCAAGTGGCATGTTTCCA 1440
QY 464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483
Db 1441 CACTGGGTATTGTTGGTCTGAGTGAATGAAAGTTTTCGGGATGTTGTTGAGACAGTTTCATA 1500
QY 484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503
Db 1501 AAAGGCACCGATGCTTTTCTGCTGCTTTTCTGATGATGCTCTGTGGAAGCCCAATCTG 1560
QY 504 TyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGly 523

Db 1561 TACCAG--GGAGGTAGGAAACCTTGGCACAGCATCAATTTATATGTGCGCATGATGGT 1617
Qy 524 PheThrLeuAlaAspLeuValThrTyrAsnIleLysLysTyrAsnLeuProAsnGlyGluAsn 543
Db 1618 TTTAGCTTGGCAGATTTAGTAACTTACCAACATAGAAATAACTTGGCAATGGAGAGAG 1677
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyPheAla 563
Db 1678 AATAATGATGGAGAGAAATCACAAATTACAGCTGGAACTGTGGAGAGAGAGACTTTGCG 1737
Qy 564 ArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheValCysLeuMet 583
Db 1738 AGTATCTCGGTGAAGAGACTAAGGAAACGACAGATGCGGAATTTCTTTGTTCCCTCATG 1797
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603
Db 1798 GTTTCCTCCAGGTGTCCCAATGATTTACATGGGAGATGAATATGGCCATACTAAAGGGGA 1857
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGlu 623
Db 1858 AACACACACACGATTTGCCATGACAACTATATGAACTATTTTCGGTGGGATAAAGGAA 1917
Qy 624 Gln--TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642
Db 1918 GAAGCACAATTCGACTTCTTCAGATTCGCGTATCTTATCAAGTTTCGTGATGAATGT 1977
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662
Db 1978 GAATCACTTGGCTTGAATGATTTCCCAACAGCAAGCGTCTGAGTGGCATGGTCTTCT 2037
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
Db 2038 CTTGAGATCCCAATTTGGTCTGAAACAGTCAATTTGTTGCAATTTTCTGCTGATCT 2097
Qy 683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
Db 2098 GTGAGCAAGAAATCTATGTGGCTTCAACACCGACTTATAGCCACACTTGTTCGCTA 2157
Qy 703 ProGluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAlaProTyr 722
Db 2158 CCGAATAGCCAGGATACCGATGGGAGCCATTTGTAGACAGCAAGAACCGGACCTTAC 2217
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742
Db 2218 GACTGATACACCGGATCTCCAGAGAGAGAAACGGCGATGAGCAGTATAGGCACCTTC 2277
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762
Db 2278 TTAGATGCAAAATGTGTACCAATGCTCAGTTACTCATCTCATCTTCTTCCACCA 2337

RESULT 7
US-09-938-842A-218
; Sequence 218, Application US/09338842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 218

; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-218
Alignment Scores:
Pred. No.: 0 Length: 2352
Score: 2895.50 Matches: 518
Percent Similarity: 81.08% Conservative: 82
Best Local Similarity: 70.00% Mismatches: 127
Query Match: 68.74% Indels: 14
DB: 11 Gaps: 4
US-09-674-817B-3 (1-764) x US-09-938-842A-218 (1-2352)
Qy 29 GluAlaAlaThrLysValGluAspGluGlyGluAspGluProValAlaGluAspArg 48
Db 140 GAAGAAACCAACGAGCT-GAAAATATCGCGTAGTAGAGAAACCTTTAAATCAGATAGA 198
Qy 49 TyrAlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68
Db 199 TTTTATCTCCGAT-----GGACTTCTTCTCATTTCGACCCACC 240
Qy 69 AlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeu 88
Db 241 GTCAGAGACGACGCGCTCAATTTCTCTGTTTACTCTACAACTCCGTTTCCGCTACCATC 300
Qy 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108
Db 301 TGTCTGATTTCTCTCCGATCTCCGTCAGACAAAGTACGAGGAGATTTCAGCTTGAT 360
Qy 109 ProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeuHisAsn 128
Db 361 CCATCAAGGAATAGAACTGGCCATGTTGGCATGTCTTCTGAGAGGAGATTTCAAAGAT 420
Qy 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
Db 421 ATGTTGATGGTTATAGATTGTAGTCAAGATTTCCTCTGAGAGAGTCAATTATTATGAT 480
Qy 149 ValSerAsnValValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGly 168
Db 481 TCCTCCCAACATTTTATGATCTCTAGCAAGAGCAATATTATAAGCAGAGATGAGTTGGA 540
Qy 169 ValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyr 188
Db 541 GTTTTGGAGACCTGATGATAATTGTTGGCTCAATGGCGTGTATGTATCCACCTCGTAG 600
Qy 189 SerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
Db 601 GAAGAGTTTGTGGAGAGGGGATATGCATCTGAGCTTCCACAGAAAGATCTTGTTATA 660
Qy 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
Db 661 TATGAAATGCATGTGCGAGGTTTTTACAAGCATGAGTCTAGTAAATTTGAATTCCTGGC 720
Qy 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248
Db 721 ACATACCAGGTTGTGAGAGAGCTTGACATTTGNAGAGGCTTGGGATAATTGTATA 780
Qy 249 GluLeuMetProCysHisGluPheAsnGluLeuGlyTyrSerThrSerSerSer----- 266
Db 781 GAATTAATGCATGTACGAGTTTAAATGAGTGGAGTATTACAGCTACATACAGATTG 840
Qy 267 -----LysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 841 GGAGACCACAGGGTAAATTTTGGGGTACTTACCATTTGGGTTCTTCTCGCCCATGATC 900
Qy 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
Db 901 AGATACGCATCAGCAAGCTCTCAACAAATTTGCTGGACGAGCCATAATGAATCAAAT 960
Qy 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHis 323

961 CTTGTTAAGGAGGCACATAAAGGAGAAATTGAGTAATCATGGATGCTGCTTTGAACAC 1020
Db
324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheIysGlyValAspAsnThrThr 343
Qy
1021 ACAGCCGAGAGGGAATGAAAGAGGCCCAATTTCTCAITTAGAGGAGTTGATAACAGTGC 1080
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344 TyrTyrMetLeuAlaProIysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
Qy
1081 TATTACATGCTGCTCCAAAGGCGAGTTCTATAATTAATTCAGGCTGTGTAATACATTC 1140
Db
364 AsnCysAsnHisProValValArgGlnPheIleValAsnCysLeuArgTyrTrpValThr 383
Qy
1141 AACTGCAATCATCCTGTGGTGGTCAATTCATATTCGATGCTGAGATATTTGGGTACA 1200
Db
384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
Qy
1201 GAAATCGATGTTGACGGCTTCGGCTTTGATCTTTGTTCAATCATGTCAGAGGAGCGAGC 1260
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1261 CTTTGGGATGCGACCAATGTTACGGGGCTGATGAGAGGTGCACTTGTCTCAAACTGCT 1320
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424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGly 443
Qy
1321 ACTCTATTAGTGGCTCCAGTAATGACATGATAGTAATGATCCAACTATCCCGCGT 1380
Db
444 ValIysLeuIleAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463
Qy
1381 GTTAAGCTAATAGCTGAAGCATGGGATGCGGTGGCTGTACCAAGTTGGCATGTTTCCA 1440
Db
464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483
Qy
1441 CACTGGGGTATTGGTCTCAGTGGAAATGGAATTTCCGGGATGTTGTGAGACAGTTCATA 1500
Db
484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503
Qy
1501 AAAGGCACCGATGGCTTTCTGGTGGCTTTTGTGTAATGCTCTGTGGAGGCCAATCTG 1560
Db
504 TyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGly 523
Qy
1561 TACCAG--GGAGGTAGGAAACCTTGGCACAGCATCAATTTTATATGTGCGCATGATGT 1617
Db
524 PheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543
Qy
1618 TTTACGTTGGCAGATTAGTAATTTACAAATAGATGATGCTTGGCAATGGAGAGAG 1677
Db
544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyPheAla 563
Qy
1678 AATAATGATGGAGAGAAATCACAAATACAGCTGGAATGTGGAGAGAGGAGACTTTGCG 1737
Db
564 ArgLeuSerValIysArgLeuArgLysArgGlnMetArgAsnPheValCysLeuMet 583
Qy
1738 AGTATCTCGTGAAGAGACTAAGGAAACACAGATGCGGAAATTTCTTTGTTCCCTCATG 1797
Db
584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrIysGlyGly 603
Qy
1798 GTTTCCTCAAGGTGTCCTCAATGATTACATGGGAGATGATATGGCCATACATAAGGGGA 1857
Db
604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysGlyGlu 623
Qy
1858 AACCAACACACGCTATTGGCCATGACAACTATATGAACATATTTTCGGTGGGATAAAGGAA 1917
Db
624 Gln---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642
Qy
1918 GAAGCACATCTTGACTTCTTCAGATTCGCGCTATCTTCATCAAGTTTCGTGATGATGT 1977
Db
643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662
Qy
1978 GAATCATTGGCTGAATGATTCCCAACAGCAAGCGCTCGAGTGCAGTGTCTTGTCT 2037
Db
663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
Qy
2038 CCTGAGATCCCAATTTGGTCTGAAACAGATGCTGATTTGTCATTTCTACTGTCGATTTCT 2097
Db

Qy 583 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
Db 2098 GTGAAGAAGAAATCTATGTGGCTTCAACACCACTCATTTAGCCACACTGTTTCGCTA 2157
Qy 703 ProGluArgAlaGlyArgArgTyrGluProValValAspThrGlyLysProAlaProTyr 722
Db 2158 CCGAATAGCCAGGATACCGATGGAGCCATTTGTACACAGCAGCAACCGAGCCCTTAC 2217
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742
Db 2218 GACTGCATAACACCGGATCTCCACAGAGAGAAACCGCGATGAAGCAGTAGTAGGCATTC 2277
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762
Db 2278 TTAGATGCAATGTGTACCAATGCTCAGTTACTCATTCATTCATTCCTCTCTTTCACCA 2337

RESULT 8

US-10-425-114-19788
; Sequence 19788, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Fihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)S
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19788
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-045-C7_FLI
US-10-425-114-19788

Alignment Scores:
Pred. No.: 0 Length: 1866
Score: 2820.50 Matches: 506
Percent Similarity: 94.05% Conservative: 31
Best Local Similarity: 88.62% Mismatches: 33
Query Match: 66.96% Indels: 1
DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x US-10-425-114-19788 (1-1866)

Qy 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214
Db 1 GGTGACCTACCCCTTGGGTACCATCAGAGGACCTTGTATATGAAATGCAATTCGCT 60
Qy 215 GlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVal 234
Db 61 GGATTCAAGACACACAACTCAAGCAAGAACACCCAGCAACTTACATTTGCTGTG 120
Qy 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254
Db 121 TCAAGCTTCACCATCTAAAGGAACTTGGAGTAGTGAAGTATAGAGCTAATGCCCTGCCAT 180
Qy 255 GluPheAsnGluLeuGluTyrSerThrSerSerSerLysMetAsnPheTrpGlyTyrSer 274
Db 181 GAGTTCATAGCTAGTAGTACTTCAGCTCCTCTTCGAAGATGAACCTTCGGGATATTC 240
Qy 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294
Db 241 ACATAAATTTTTCTCACCATGGCAAGATATCTTCAAGTGGCATAGAGACTCTCGGA 300
Qy 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314

Db 301 TGTGGTGCCTAAATGAATTTAAAGCTTTTGAAGGGAGGCCCAAAACGGGGAATTGAG 360
Qy 315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334
Db 361 GTGATCATGGATGTTGCTCTCAATCATACAGCTGAAGGTATGAGAAAGGCCCAATATTA 420
Qy 335 SerPheLeuGlyValAspAsnThrThrTyrrMetLeuAlaProLysGlyGluPheTyrr 354
Db 421 TCTTTAGGGGATAGATAATAGTACTACTACTACTACTACTACTACTACTACTACTACT 480
Qy 355 AsnTyrrSerGlyCysGlyAsnThrPheAsnHisPheAsnHisPheValValArgGlnPheIle 374
Db 481 AATTATCTGTTGTTGGAATACCTTCAATGTATATCATCTCTGTAGTCCGTGAATTTATA 540
Qy 375 ValAspCysLeuArgTyrrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu 394
Db 541 GTGGATTGCTTGCAGATACCTGGTAAACAGAAATGCAATGTATGATCTCTGTAGTCCGT 600
Qy 395 AlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrrGlyValPro 414
Db 601 GCATCTATCTACTGACACAGAGATGCAAGTCTATGCGGATCCAGTTAATGTATGGAAGTCCA 660
Qy 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMet 434
Db 661 ATGGAAGTGCATGATGATACGACAGGACACCTCTGTTGCCACCACTTATTGACATG 720
Qy 435 IleSerAspAspProIleLeuGlyValIleLeuAlaGluAlaTrpAspAlaGly 454
Db 721 ATTAGCAATGCCCAATCTTGGAAATGCAAGCTCAATGCTGAAGCATGGGATGCAGGA 780
Qy 455 GlyLeuTyrrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474
Db 781 GGTCTCTATCAAGTTGGTTCAGTTCTCTCACTGGAAGCTTTGGTCAGAGTGAATGGAAG 840
Qy 475 TyrArgAspIleValArgGlnPheLeuLysGlyThrAspGlyPheAlaGlyGlyPheAla 494
Db 841 TATCGGATACCGTGGCTGATGTTCAATCAAGACAGAGATGGATTTGCTGGTCTTTTCT 900
Qy 495 GluCysLeuCysGlySerProHisLeuTyrrGlnAlaGlyGlyArgLysProTrpHisSer 514
Db 901 GAATGCTATGTGAAGTCCACAGTTATACAGGACGAGGGGAGGAGGAGCTTGGACAGT 960
Qy 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrrAsnLys 534
Db 961 ATCAACTTTGTATGTCACACAGATGATTTACACTGGCTGATTTGGTCACATACATAAGC 1020
Qy 535 LysTyrrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp 554
Db 1021 AAGTCAACTTGTCAATGTTGAGGACACAGATGGGAAATCATATCTTACCTGCG 1080
Qy 555 AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574
Db 1081 AATTGTGGGAGGAGAGAAATTTGCAAGTCTGTCAGTCCGAAGATTAAGGAAGAGGCAA 1140
Qy 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrrMetGly 594
Db 1141 ATGCGCAATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1200
Qy 595 AspGluTyrrGlyHisThrLysGlyLysAsnAsnThrTyrrCysHisAspSerTyrrVal 614
Db 1201 GATGATATGTTGTCACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Qy 615 AsnTyrrPheArgTrpAspLysLysLysLysLysLysLysLysLysLysLysLysLys 633
Db 1261 AATTATTTCCGTTGGGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Qy 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAla 653
Db 1321 CTATGACCAATTCGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Qy 654 LysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArg 673

Db 1381 GRACGGTTGAATGGCAACGGTTCATCAGCCCGGGAAGCCCTGACTGCTGAGAGGCAAGCCGA 1440
Qy 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrrValAlaPheAsnThr 693
Db 1441 TTCGTTGGCTTCCACCATGAAGACGAACCAAAAGGCGAGATCTAGTGGCCCTTCAACACC 1500
Qy 694 SerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgTrpGluProVal 713
Db 1501 AGTCACCTTCGGTGGTTCCTGAGAGCGCTCTGGGTTCCGATGGGAGCGGTG 1560
Qy 714 ValAspThrGlyLysProAlaProTyrrAspPheLeuThrAspAspLeuProAspArgAla 733
Db 1561 GTGACACCGGCAAGGAGGACCATATGACTTCTCCACCATGGCTGCCAGATCGTGCT 1620
Qy 734 LeuThrIleHisGlnPheSerHisPheLeuTyrrSerAsnLeuTyrrProMetLeuSerTyrr 753
Db 1621 GTCACCGTTCACAGTCTCTCATTTCTCAACTCCAACTCTATCTATCTATGCTCAGCTAC 1680
Qy 754 SerSerValIleLeuValLeuArgProAspVal 764
Db 1681 TCCTCCATCATCCTCTGTTATTTGGCCCTGATGTC 1713

RESULT 9
US-09-850-936-1
; Sequence 1, Application US/09850936
; Publication No. US20030167527A1
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/850,936
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US/09/187,124
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/EP97/02292
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: DE 196 18 125-9
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1819)
; OTHER INFORMATION: Clone: Iso5
US-09-850-936-1
Alignment Scores:
Pred. No.: 5,31e-309 Length: 2133
Score: 2612.00 Matches: 460
Percent Similarity: 86.86% Conservative: 62
Best Local Similarity: 76.54% Mismatches: 73
Query Match: 62.01% Indels: 7
DB: 10 Gaps: 2
US-09-674-817B-3 (1-764) x US-09-850-936-1 (1-2133)
Qy 166 GluTyrrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIlePro 185
Db 1 GATTTGGCCAGGAGGCCAGAGGAT--GATTGTTGGCCCCCATGCGCAGCATGGTACCT 58
Qy 186 LeuProTyrrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrrProGlnLysAsp 205
Db 59 TCTGCTTCTCATCAGTTTGATTGGGAGGAGATCTATTACTGAAGTTTCCACAGAGAT 118
Qy 206 LeuValIleTyrrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu 225
Db 119 CTGTATATCTATGAATGATGATGTTGTTGATTTTACAAATCATGAGTCGAGTGAACACAAA 178

US-09-674-817B-3 (1-764) x US-10-425-114-6193 (1-1830)

QY 289 GlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAla 308
Db 4 GGCATACGAACTGTGGCCAGGATTAATGAATTAATCTCTGATCAAGAGCG 63

QY 309 HisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsn 328
Db 64 CACAAACCGAGGAATAGAGTCAATGATGATGTTTTCATATACAGCTGAGGGGAAT 123

QY 329 GluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAla 348
Db 124 GAGATGTGTCCTATTTCTTCAGAGGTGCGACACAGTATGTTATACATGTAGCA 183

QY 349 ProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPro 368
Db 184 CCCAAGGGGAGTCTCTAATACTATTTCAGGATGTGGAAACAGCTTCAATTGCAACCATCCA 243

QY 369 ValValArgGlnPheIleValAspCysLeuArgTyrTyrValThrGluMetHisValAsp 388
Db 244 GTGTGCGCAATTTATAGTTGCTTACGATTTGGTAAACGAAATGCACTGGAT 303

QY 389 GlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspProVal 408
Db 304 GGTTCCTGCTTGTGCTTCTATATGACGAGGATGACAGTCTCTGGGATGGAGCT 363

QY 409 AsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428
Db 364 AATGATTTTGGTCTCCCAATAGAGTCACTTGTGGAAACAGGAAACCTCTTAAGCAGC 423

QY 429 ProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuAla 448
Db 424 CCACCATTAATTTGACTTGATCAGTACGATCCTATACCTTTGGAGTGAAGCTTATAGCT 483

QY 449 GluAlaThrPheAlaGlyLeuTyrGlnValGlyGlnPheProHisThrPheAsnValThr 468
Db 484 GAAGCTGGGATGCTGTGCTCTATCAAGTTGCTCTTCCCTCACTGGGGTATTTGG 543

QY 469 SerGluThrAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGly 488
Db 544 TCAGATGGAATGGGAGTATAGACACGCTGCGCTGTTTATCAAGGATACAGATGCG 603

QY 489 PheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGly 508
Db 604 TTTGCTGGAGCTTTGCTCAATGCTTGTGGAGTCTCTAATTTATATCAGGAGGAGGA 663

QY 509 ArgLysProThrPheSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAsp 528
Db 664 AGAAACCGTGGATAGTATTAATTTGATCGCTCATGATGGTTCTCTAGCTAGTAT 723

QY 529 LeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGlu 548
Db 724 TTGGTCACTATAACAAAGAAATTAATTTGTCAATGGAGAGACAAATATGATGAGAA 783

QY 549 AsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLys 568
Db 784 AATCATATAATAGCTGGAACTGCGGACAGGAGGGGAGTTTGTCAAGTACCTTCGGGTGAAG 843

QY 569 ArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVal 588
Db 844 AATTCAGGAACAGCAATAGCGGAATTTTCTCTCTCATGTTTCCCGAGGAGTT 903

QY 589 ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyCysAsnAsnThrTyr 608
Db 904 CCAATGATATATATGGGCGGATGAATGATGACACACAAAGAGGAGGAATTAACAAATACCTAT 963

QY 609 CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGln---TyrSerGlu 627
Db 964 TGTCACGATAATTTATCATATTTCTTCCATTTGGGACAAAAGAGGAATTCCTCATCAGAC 1023

QY 628 LeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeu 647
Db 1024 TTCTTCAGATTTTGTGCTTATGACTAAGTTCCCGCAGGAATGTGAATCGCTAGGCTTA 1083

QY 648 GluAspPheProThrAlaLysArgLeuGlnThrHisGlyHisGlnProGlyLysProAsp 667
Db 1084 GCTGACTTCCCAACTCTGAGAGGCTGCAGTGGCATGGTCAATTTCTTGGAAAGCCAGAC 1143

QY 668 TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIle 687
Db 1144 TGGTCTGAAACACGCGCTTTTGTGGCTTACCATGGTAGATTTCAGTGAAGGAGAAATA 1203

QY 688 TyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly 707
Db 1204 TACATTCGCTTCAATATAGTATTCATTTACCTTTACAGTTCCTTCCCGAGCGTCTGGA 1263

QY 708 ArgArgTyrGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAsp 727
Db 1264 TACAATGGAACTCTTGTAGACACGACGCTTACACCATATGATTTCTCTACTCT 1323

QY 728 AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu 747
Db 1324 GACCTTCCTGGAAGAGATATTCATATACACAGTATGCTCAGTTTCTGACGCCAATATG 1383

QY 748 TyrProMetLeuSerTyrSerSerValIleLeuValLeuArgProAsp 763
Db 1384 TATCCCATGCTTAGTTATTTCTTCATATTCCTTCCTTCGCGCATCCAGAT 1431

RESULT 11

US-10-424-599-11817
; Sequence 11817, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 39-21(53223)/B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 11817
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110679C.1

US-10-424-599-11817

Alignment Scores:
Pred. No.: 8,496-253 Length: 2052
Score: 2153.50 Matches: 381
Percent Similarity: 88.03% Conservative: 56
Best Local Similarity: 80.04% Mismatches: 56
Query Match: 51.13% Indels: 1
DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x US-10-424-599-11817 (1-2052)

QY 289 GlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAla 308
Db 4 GGCATACGAACTGTGGCCAGGATTAATGAATTAATCTCTGATCAAGAGCG 63

QY 309 HisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsn 328
Db 64 CACAAACCGAGGAATAGAGTCAATGATGATGTTTTCATCATACAGCTGAGGGGAAT 123

QY 329 GluAsnGlyProIleLeuSerPheLysGlyValAsnThrThrTyrTyrMetLeuAla 348
Db 124 GAGATGTGTCCTATTTCTTCAGAGGTGTCGACACAGTATGTTATACATGTAGCA 183

QY 349 ProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPro 368
Db 184 CCCAAGGGGAGTCTCTAATACTATTTCAGGATGTGGAAACAGCTTCAATTCACCATCCA 243

QY 369 ValValArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAsp 398
Db 244 GTTGTGGCAACATTTATAGTTGACTGCTTAAAGATATTGGTAAACAGAAATGCACGGAT 303
QY 389 GlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProVal 408
Db 304 GGTATTTCCGCTTTCATCTTCTCTTATATGACACAGGAGTAGCAGTCTCTGGGATGGAGCT 363
QY 409 AsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428
Db 364 AATGTATTTGGTGCTCCAAATAGAGGAGTCTTGTTCACACAGGAAACCCCTCTAAAGCAGC 423
QY 429 ProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuAla 448
Db 424 CCACCATTAATGACATGATCAGTAACGATCCTATATCTTGTGGAGTAGAGTTATAGCT 483
QY 449 GluAlaTrpAspIleGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrp 468
Db 484 GAAGCTGGGATGCTGGTGCCCTTATCAAGTTGGCATTTCCTCACTGGGCTATTGG 543
QY 469 SerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGly 488
Db 544 TCAGATGGAATGGGAGATAGACACAGTGGCGCTGTTTATCAAGGATACAGATGC 603
QY 489 PheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGly 508
Db 604 TTTGCTGGAGCTTTGCTGAATGCCCTTGTGGAGTCCTAAATTTATATCAGGAGGAGGA 663
QY 509 ArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAsp 528
Db 664 AGAAACCGTGGCATAGTATTAACTTTGTATGGCTCATGATGGGTTCACCTACCTGAT 723
QY 529 LeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGlu 548
Db 724 TTGGTGACCTATAACACAGAAATAATTTGTCAATGGAGAGACAAATAATGACGAGA 783
QY 549 AsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLys 568
Db 784 AATCATATAATAGCTGGAACTGGCGACAGGAGGGGGAGTTTGTGAGTACCTCGGTGAAG 843
QY 569 ArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVal 588
Db 844 AAATGGAGAAACGACAAATGGGAATTTTCTTCTCATGCTGTTCCAGGGAGTT 903
QY 589 ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyr 608
Db 904 CCAATGATATATATGGCGATGAATATGACACACAAAGAGGAGAAATAACAAATACCTAT 963
QY 609 CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGln---TyrSerGlu 627
Db 964 TGTCAGATATATCATATTTACTTCCAATGGGACAAAGAGAAATCCTCATCAGAC 1023
QY 628 LeuHisArgPheCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeu 647
Db 1024 TTCTTCAGATTTTGTGCTTATGACTAAGTTCCGCGAGGATGTGAATCCTAGGCTTA 1083
QY 648 GluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAsp 667
Db 1084 GCTGACTTCCCAACCTCTGAGAGGCTGCAGTGGCATGTGCTATTTTCTCGGAAAGCCAGAC 1143
QY 668 TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyLeuIle 687
Db 1144 TGGTCTGAACACGACCGTTTGTGGCTGTACCATGTTAGATTACGTGAAGGGAGAAATA 1203
QY 688 TyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly 707
Db 1204 TACATGTGTTCAATATGATGATTTACCTTTTCAGTTTACCTTTCGCGGAGCGTCTGGA 1263
QY 708 ArgArgTyrGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAsp 727
Db 1264 TACAATGGGAACCTCTTGTAGACACAGCAGGCTTACCATATGATTTTCTCCTCACCTCT 1323

QY 728 AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu 747
Db 1324 GACCTTCCTGGAGAGATATTGCCATACACAGATATGCTCAGATTCTTCGACGCCAATATG 1383
QY 748 TyrProMetLeuSerTyrSerValIleLeuValLeuArgProAsp 763
Db 1384 TATCCATGCTTAGTTATTCTTCATTATCTCTTGCGCATTCAGAT 1431
RESULT 12
US-10-369-493-26385
; Sequence 26385, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26385
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Synecocystis sp.
US-10-369-493-26385
Alignment Scores:
Pred. No.: 1,36-189 Length: 2124
Score: 1636.50 Matches: 342
Percent Similarity: 60.20% Conservative: 77
Best Local Similarity: 49.14% Mismatches: 216
Query Match: 38.90% Indels: 61
DB: 16 Gaps: 16
US-09-674-817B-3 (1-764) x US-10-369-493-26385 (1-2124)
QY 56 ArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsn 75
Db 46 AAATCGCTGTGCCAGCCCTTCCCTTTGGGCCACCATTTGTCGGGGGAGTTAAT 105
QY 76 PheAlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAsp 95
Db 106 TTTTCCATTACTAGCCATAGCCGCTTGACCCCTAGTACTGTC-----GAG 156
QY 96 LeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115
Db 157 AAGCGGCTCCCGAGCCCTTTGTGGAGATTCCTTT---CCAGAACTTTTCGCAATGGT 213
QY 116 AsnValTrp---HisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArg 134
Db 214 AATGCTATTGCAATGCTGTGTGTTGACCTGGATTTTGAGAACTCTGGAATACGCTATCGC 273
QY 135 PheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValVal 154
Db 274 ATGGAAGGCCCAATAACTTCCAGAGGCCCATTTGTTTGCACCCAGTAAGTTCCTTCT 333
QY 155 AspProTyrAlaLysAlaValIleSerArgGlyGlyTyrGlyValProAlaArgGlyAsn 174
Db 334 GATCCCTACGCCAAAGTGTGTCAGTGGCGGGATGTTTGGGGCACCCACCAATTCGGAC 393
QY 175 AsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGlu 194
Db 394 GATATTAT---CAACACCGGGGCCGC-----CTCAGCTTTGACAAATTTGATTGGGAA 444
QY 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214
Db 445 AACGATTTCCCTCGTATGTTCCCTTCGAAGACATGCTCATTTATGAAATGCAATGTCGCG 504

```

568 LysArgLeuArgLysArgGlnMetArgAsnPheValCysLeuMetValSerGlnGly 587
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1519 CTCAGACTCCGGCCCGCAATTCGGAATCGCATTTTGTGGTGATGTCAGGGG 1578
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
588 ValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThr 607
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1579 GTGCCCATGCTGTGTGGAGACGNAATGGGCAAAACCCAGACGCGCAACATAATACC 1638
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
608 TyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluInTyrSerGlu 627
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1639 TATTGCCACGATTCCTTCAATTGGCTCAATTGGCATTTACTTGACAAACACAGGCT 1698
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
628 LeuHisArgPheCysCysLeuMetThrLysPheArg----- 639
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1699 TGGTTTCGGTTGTCAAACTGCGATGCTTCCGCTAGCCACCCTGATTACGCAAC 1758
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
640 -----LysGluCysGluGlyLeuGlyLeuGluLeuAspPheProThrAlaLysArg 655
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1759 AGTGAACATTTCCAAAACCTGCGATTACCTTGGTGTG--GGATTTCCCGAT-- 1806
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
656 LeuGlnTrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheVal 675
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1807 ATTAGTTGGACAGGAGTCAGCCCTGGCACGCTGACTGTCCGCGATGCGCGAGTTTA 1866
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
676 AlaPheSerMetLysAspGlu-----ArgGlnGlyGluIleTyr 688
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1867 GCTTTTATGCTTTGTGTGCCCATGCCAAAGGTGGCCGAGTTAAGGATAAATCAAAATTTAT 1926
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
689 VallAlaPheAsnThrSerHisLeuProAlaValValGluLeuPro--GluArgAlaGly 707
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1927 GTGGCCCATGAATATGCAATTACGAAAGTCTTTTGGTTTGAACCTGCCAGCTCCCGGTGGC 1986
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
708 ArgArgTyrGluProValValAspThrGlyLysProAlaProTyrAsp 723
      |||...|||...|||...|||...|||...|||...|||...|||...|||...
1987 ACCACTGGCACGTTTTCGCCACACAGGGGCCAGCTCCAGAAGAT 2034
      |||...|||...|||...|||...|||...|||...|||...|||...|||...

RESULT 13
US-10-437-963-39232/c
; Sequence 39232, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with Rice
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 39232
; LENGTH: 2729
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42793C.1
US-10-437-963-39232

Alignment Scores:
Pred. No.: 5,24e-179 Length: 2729
Score: 1553.50 Matches: 343
Percent Similarity: 56.75% Conservative: 111
Best Local Similarity: 42.88% Mismatches: 256
Query Match: 36.88% Indels: 88
DB: 17 Gaps: 22

US-09-674-8178-3 (1-764) x US-10-437-963-39232 (1-2729)

```

QY 2 GlyProAlaProArgLeuArgArgTrpArgProAsnAlaThrAlaGlyLysGlyValGly 21
Db 2694 GGGCGGCTCCG-----TGGAAAGTGGGTGGCGAGCATGGCTTCGGG 2647
QY 22 GluValCysAlaAlaValValGluAlaAlaThrLys----- 33
Db 2646 GAC-----CGGTCTGGGCTCAGAGCGGTCTCGAAGAGCGAGTTAGCGGATTTGATTTC 2593
QY 34 ---ValGluAspGluGlyGluAspGluProValAlaGluAspArgTrpAlaLeuGly 52
Db 2592 TGTACGAAGCACCACCGGAGAGCTCAGAACGGGACGCTGGGAGAGCATGCCAGGA 2533
QY 53 -GlyAlaCys-----ArgValLeuAlaGlyMetProAl 63
Db 2532 AAGAGGATGACAAATGTCTGATACTGAAATGCCATTTAAATATTTCTCTGTAAGACCTT 2473
QY 63 aProLeuGlyValAlaThrAlaLeuAlaGlyValAsnPheAlaValTyrSerGlyGlyAl 83
Db 2472 CCATTTAGGAGTCTCTCAAGTTCAAGCGGCTGAACTTCGCACATTTCTCTCAGCATGC 2413
QY 83 aThrAlaAlaLeuCysLeuPheThrPro-----GluAspLeuLysAlaAs 99
Db 2412 TTCTTCTGTCATTTCTGCTTAAAGCTTCTGGAGGGGAACTGAAGATGAGAAAGGTGC 2353
QY 99 pArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHi 119
Db 2352 AGATGTTGCGAGTTGTT---TTAGACCAGCAGAAAGCAAACTGGCGATATATGGCA 2296
QY 119 sValPheIleGluGly---GluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyTh 138
Db 2295 TGTGATAGTGGAGGCTTGCTGCTTCTGCTGTTCTTTATGGTATCGTGTGGTGGCCC 2236
QY 138 rPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAl 158
Db 2235 TCAAGGATGGGACCAAGGCCATAGATTGTATGACGACACTGTCTTCTGACCCCTATGTC 2176
QY 158 aLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpPr 178
Db 2175 AAAATTAGTTCTGCTGCGAAAGTACTTTGGGGTTGCTGAAGAGAAGTCAAGC----- 2124
QY 178 oGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuPr 198
Db 2123 -CAGCATTTTGGAAATATGATTTTATGATAGCTCTCTTTGATTTGGGTGATGACTACAG 2065
QY 198 oLeu---ArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheTh 217
Db 2064 GTTTCGAATTGCTTGAGCGAGATCTAGTCATATGAAATGAACGCTCCGTCCTTAC 2005
QY 217 rLysHisAspSerSerAsnValGluHisPro-----GlyThrPheIleGlyAlaValSe 235
Db 2004 CGCGATGAGTCAAGTGGCTTTGATTCGACTTCTCGTGAAGCTATCTTGGTCTCATTTGA 1945
QY 235 rLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGl 255
Db 1944 TAAATCCCTCATTTTCTGCTGAACTTGGCGTTAATCAGTGAACACTCTCTCTGTTTTTGA 1885
QY 255 uPheAsnGluLeuGluTyr-----SerThrSerSerSerLysMetAsnPheTr 271
Db 1884 GTATGATGAGCTGGAAATTCAGAGGTACCCCAACCAAGGACCATATGGTCAATACATG 1825
QY 271 pGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLy 291
Db 1824 GGGCTATTCTACGATAAACTTTTTCGCCATGAGCCGTTATGCTAGTGGCGGTGGTG 1765
QY 291 sAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysAr 311
Db 1764 ACCAGTGGCT-----GCTTCCAAAGAGCTCAAGCAGATGGTCAAGAAATGCTATAAGC 1711
QY 311 gGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGl 331
Db 1710 TGGCATAGAGTTATTCTTGGATGTTGTTTACAAACCATACAAATGAGCGGATGATGCTCA 1651
QY 331 yProIleLeu---SerPheLysGlyValAspAsnThrThrTyrTyrMet-----LeuAl 348

Db 1650 CCCGTATATGACTCTTTCCTGGCATGTATGAAAGGTCTATTACATGTTAGACCTGAA 1591
QY 348 aProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPr 368
Db 1590 CAAAAATCTGAACCTACTGAACCTTCTCAGGCTGGGGAATACACTGAACCTCAACCATCC 1531
QY 368 oValValArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAs 388
Db 1530 TGTGTCAAGAGAGCTCATCTTGACAGCTTGAGACACTGGGTGAGGAGTATCACATAGA 1471
QY 388 pGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProVa 408
Db 1470 TGGATTTGCAATTCACCTTGCAAGTGTCTTGTTCGTGGACCAT----- 1425
QY 408 lAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValTh 428
Db 1424 -----CGTTGTCTCTTTGATGC 1408
QY 428 rProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuIleAl 448
Db 1407 ACCTCCACTCATCAAGGAAATTCCAAAGATGCTGTATTATCTAGATGTAAGATCATTGC 1348
QY 448 aGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTr 468
Db 1347 TGAACCTTGGGATTCGCGCGCTTTATCTCGTAGGCGCTTCCCTAACTGGGACAGGTG 1288
QY 468 pSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGl 488
Db 1287 GGCTGAATGGNACGGCAATACAGAGATGATCTTCGAAGATTATTAAAGGTGACCTGG 1228
QY 488 yPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGl 508
Db 1227 TATCAAGGGGTGTTTCGACTCTGTGCTGTGATCTGCTGATCTATCAGGTGAACGA 1168
QY 508 yArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAs 528
Db 1167 GCGAAGCCCTTACCATGGTGTAAATTTGTGATTGTCACATGATGATGATTTACTTTATGTA 1108
QY 528 pLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGl 548
Db 1107 CCTTGTCTTACAACTTAAAGCAATATGATGCTTAATGGAGAGGTGGCTGTGATGATG 1048
QY 548 uAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLy 568
Db 1047 CAATGACAATTTAGCTGGAACTGTGGTGTGAAGGAGAAACAAATGATCTGAATGTGTT 988
QY 568 sArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVa 588
Db 987 AAGTCTCGCTTCAAGACAAATGAAACCTTCCATGATAGCTTTAATGATTTCTCAGGCGAC 928
QY 588 lProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTy 608
Db 927 CCCAATGATGTTGATGGCGCATGATATGTTTCATACACGTTATGGGAACAACAATAGCTA 868
QY 608 rCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLe 628
Db 867 TGGNATGATACTTGTCAATTAATTTCCATGGGACAGTTGGAAACAAGAGAGAGATGG 808
QY 628 uHis---ArgPheCysCysLeuMetThrLysPheArgLysGluCysgludlyLeuGlyLe 647
Db 807 CCATTTTCAGGTTTTTCTCAGAGATGATAAAGTTTCGTCACAGCAACCAATATTAAAGCG 748
QY 647 uGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAs 667
Db 747 AGACAGGTTTTTAAATAAAACGATGTCACCTGGCAC-----GAGGATTG 703
QY 667 pTrp---SerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGln---Gl 685
Db 702 TTGGGAGAACCGAAGCAAAATTTTGGCAATTCACAGTACATGATCAACAACCTCGGTGG 643
QY 685 yGluIleTyrValAlaPheAsnThrSer-----HisLeuProAlaValValGluLeuPr 703

Db 642 AGATATCTATTGGGCAATCAATGACATGACTATTTTGTGACCGCTGTAATTCCTCCACC 583
 Qy 703 ogluargalaglyArgArgTTPGluProValValAspThrGlyLysProAlaProTyrAs 723
 Db 582 ACCACAC---CATAAATGTTGAACCGTGTGTGATACCAACCTGGGAATCACCAATGA 526
 Qy 723 pphleuthrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLe 743
 Db 525 TATTGTACAGAAAGGGTGCCA-----TT 502
 Qy 743 uTyrSerAsnLeuTyrProMetLeuSerTyrSerValIleLeuValLeuArgPro 762
 Db 501 TACAGGACCAAAATACAGAAATGCTCCATCTCTCCATTTCTGCTCAAGGCAAGCCT 444

RESULT 14
 US-10-425-114-20367
 ; Sequence 20367, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yinhua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 20367
 ; LENGTH: 1198
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3180-047-B3_FLI
 US-10-425-114-20367

Alignment Scores:
 Pred. No.: 2,75e-176 Length: 1198
 Score: 1526.50 Matches: 279
 Percent Similarity: 88.82% Conservative: 15
 Best Local Similarity: 84.29% Mismatches: 19
 Query Match: 36.24% Indels: 19
 DB: 13 Gaps: 2

US-09-674-817B-3 (1-764) X US-10-425-114-20367 (1-1198)

Qy 452 AspAlaGlyLeuTyrGlnValGlyGlnPheProHisTyrAsnValTyrSerGluTyr 471
 Db 3 GATCGAGGAGTCTATCAAGTTGTCAGTTTCTCTCACTGGACGTTTGGTCAAGATGG 62
 Qy 472 AsnGlyLys----- 474
 Db 63 AATGGAAA-GGCCAACCTTAGAGTATGTTTCAAAACATAGCCTCACTGACCAATAG 121
 Qy 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyPheAla 494
 Db 122 TATCGGATACCGTGCCTCAGTTTCATCAAGGACAGATGGATTTGCTGGTCTTTGCT 181
 Qy 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProThrHisSer 514
 Db 182 GAATGCTATGTGAAGTCCAGTTATACAGAGGGGGGAGGAGCCTTGGCAGAT 241
 Qy 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534
 Db 242 ATCACTTTGTATGTGCACACGATGGATTTACACTGCTGATTTGTCACATACATAGC 301
 Qy 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyr 554
 Db 302 AAGTACAACCTGTCAAATGTTGGAGCAACAGAGATGGGGAATCATATCTTAGCTGG 361

Qy 555 AsnCysGlyGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574
 Db 362 AATTGTGGGAGGAGGAGAAATTTGCAGTCTGT CAGTCCGAAGATTAAAGGAAGAGCAA 421
 Qy 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
 Db 422 ATCGCAATTTCTTTGTTGTTTCTTCAAGGAGTTCCAAATGTTTACATGGC 481
 Qy 595 AspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrVal 614
 Db 482 GATGAATATGTCACAAAGGAGGAGAAACAATACGTACTGTCATGACCATATATGTC 541
 Qy 615 AsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633
 Db 542 AATTATTTCCGTTGGATTAAGGAAGAAACAATCTCTGATTGTACAGATTCTCCGT 601
 Qy 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAla 653
 Db 602 CTCATGACCGAATTCGCCAAAGAAATGTGAATCTCTTGGCCTTGAGGACTTCCGACTTCA 661
 Qy 654 LysArgLeuGlnThrHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArg 673
 Db 662 GAACGGTTGAAATGGCACCGTCAACAGCCCGGGAAGCCTGCTGGTCAAGGCAAGCGA 721
 Qy 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThr 693
 Db 722 TTGCTTGCCTTCAACCATGAAGGACGAAACCAAGCGAGATCTAGTGGCCTTCAACACC 781
 Qy 694 SerHisLeuProAlaValGluLeuProGluArgAlaGlyArgArgTyrGluProVal 713
 Db 782 AGTCACTTCCGTTGTTGTTGGCTTCCAGAGCGCTCTGGGTCGATGGGAGCGGCGTG 841
 Qy 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733
 Db 842 GTGGACACCGGCAAGGAGGACCATATGACTTCTCCTCAGCGATGGCCTGCGCATCTGCT 901
 Qy 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753
 Db 902 GTCACCGTCTACAGTCTCTCTATTTCTCAACTCCAACTCTATCTATGCTTACGCTAC 961
 Qy 754 SerSerValIleLeuValLeuArgProAspVal 764
 Db 962 TCCTCCATCATCTCTGTTATTTGGCCCTGATGTC 994

RESULT 15
 US-10-369-493-26296
 ; Sequence 26296, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 26296
 ; LENGTH: 2241
 ; TYPE: DNA
 ; ORGANISM: Synecocystis sp.
 US-10-369-493-26296

Alignment Scores:
 Pred. No.: 7.5e-159 Length: 2241
 Score: 1389.00 Matches: 305
 Percent Similarity: 53.86% Conservative: 86
 Best Local Similarity: 42.01% Mismatches: 251

Db 2080 TTGGAATTGCCCCCTCTAAACGATGTTTGATTGGCATCGACTGGTGGATACCTATTTA 2139
Qy 719 ProAlaProTyrAspPhe 724
Db 2140 CCAACTCCGTTGGACTTC 2157

Search completed: August 10, 2004, 07:28:27
Job time : 1509 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2004, 00:45:10 ; Search time 4809 Seconds
(without alignments)
4744.168 Million cell updates/sec

Title: US-09-674-817B-3
Perfect score: 4212
Sequence: 1 SGPAPLRWRNRNATAGKV.....SNLYPMLSYSSVILVLRPDV 764

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh
-Q/cgn2_1/USFT0_spool/US09674817/runat_04082004_165844_24593/app_query.fasta_1.903
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0
-UNIT3=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674817@cgn.1.1.3437@runat_04082004_165844_24593 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_ptg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	1201	28.5	910	13	BQ609719	BQ609719 BRY 5805
C 2	1117	26.5	737	13	BQ609582	BQ609582 BRY_5559
C 3	1092	25.9	625	14	CD897205	CD897205 G174.105C
C 4	1074	25.5	617	13	BQ997255	BQ997255 HI07G18r
C 5	1053.5	25.0	655	14	CB035933	CB035933 VVA015B02
C 6	1052	25.0	590	12	BQ267405	BQ267405 BJ267405
C 7	1038.5	24.7	913	12	BQ444934	BQ444934 GA_Ra002
C 8	998.5	23.7	753	13	BQ65760	BQ65760 QGC5M22.Y
C 9	986	23.4	578	10	BE493792	BE493792 WHE1275.E
C 10	981	23.3	637	14	CA781552	CA781552 024A03AF
C 11	974.5	23.1	697	14	CA199345	CA199345 SCRLFL101
C 12	948.5	22.5	661	13	BQ039907	BQ039907 PP_LBa000
C 13	943.5	22.4	622	14	CF041929	CF041929 QCT31h03.
C 14	943	22.4	536	13	BQ971724	BQ971724 HB19H15r
C 15	904	21.5	519	13	BQ970613	BQ970613 HB15C17r
C 16	894	21.2	508	14	CD890597	CD890597 G118.115A
C 17	885.5	21.0	591	14	CB605134	CB605134 3529_1.68
C 18	885	21.0	785	12	BJ591026	BJ591026 BJ591026
C 19	866.5	20.6	551	14	CB617184	CB617184 3529_1.70
C 20	863.5	20.5	644	9	AI737641	AI737641 605036B10
C 21	853.5	20.3	582	13	BU043560	BU043560 PP_LBa001
C 22	843	20.0	564	12	BU272361	BU272361 BU272361
C 23	818.5	19.4	759	12	B1176864	B1176864 EST517809
C 24	816	19.4	729	12	BQ595165	BQ595165 BJ595165
C 25	814.5	19.3	592	12	B1934640	B1934640 EST554529
C 26	810.5	19.2	580	12	B1934559	B1934559 EST554448
C 27	810.5	19.2	712	14	CD442228	CD442228 EL01N0437
C 28	803.5	19.1	550	13	BU090334	BU090334 8x70803.Y
C 29	766	18.2	445	13	BU974414	BU974414 HB27N18r
C 30	764	18.1	438	13	BU971450	BU971450 HB17K14r
C 31	761.5	18.1	967	14	CK291085	CK291085 EST753799
C 32	756.5	18.0	558	10	AW832588	AW832588 sm14507.Y
C 33	753	17.9	438	13	BU971179	BU971179 HB16N12r
C 34	747	17.7	431	12	BM500514	BM500514 PAC000000
C 35	745.5	17.7	496	14	CF040681	CF040681 QCI17A05.
C 36	743.5	17.7	547	12	BM178903	BM178903 saj60R07.
C 37	738.5	17.5	497	14	CD442761	CD442761 EL01N0417
C 38	730.5	17.3	473	14	CK101133	CK101133 F023P78.5
C 39	717.5	17.0	781	14	CD576563	CD576563 UCRPT01.0
C 40	703.5	16.7	669	14	CD003812	CD003812 VVA015B02
C 41	703	16.7	469	12	BI075394	BI075394 IP1_20.A0
C 42	702	16.7	392	13	BU973837	BU973837 HB26B22r
C 43	696	16.5	584	14	CB877804	CB877804 HP06B23T
C 44	682.5	16.2	574	9	AI901664	AI901664 618008G03
C 45	682	16.2	474	14	CD890598	CD890598 G118.115A

ALIGNMENTS

RESULT 1
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LOCUS BQ609719
DEFINITION BRY 5805 wheat EST endosperm library Triticum aestivum cdna 5', mRNA sequence.
ACCSSION BQ609719
VERSION BQ609719.1 GI:21559058
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

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REFERENCE 1 (bases 1 to 910)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
FEATURES
    source
        1..910
            /organism="Triticum aestivum"
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Pred. No.: 4,02e-123 Length: 910
Score: 1201.00 Matches: 235
Percent Similarity: 92.11% Conservative: 10
Best Local Similarity: 88.35% Mismatches: 14
Query Match: 28.51% Indels: 7
DB: 13 Gaps: 0
US-09-674-817B-3 (1-764) x BQ609719 (1-910)
QY 79 TyrSerGlyGly-AlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAl 98
DB 786 TATTCGAGGAGGAGCCAAATAGGAGGATATGCTTATTCAGCCAAAGATCTCAAGC 727
QY 98 aAspArg-ValThrGluGluValProLeuAspProLeuMetAsnArgThr-GlyAsnVal 117
DB 726 GAATAGGGGTTCACAGGAGGTCCTTGCCTTATGATCGGACCGGGGAAGGTG 667
QY 118 TrpHisValPhe-IleGluGlyGluLeuHisMetLeuTyrGlyTyrArgPheAspGl 137
DB 666 TGCCATGTTTTCATGGAAGGCAAGCTGCACACATACTTAAACGGGAACAGGTCGACGG 607
QY 137 YThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnVal-ValValAspProT 157
DB 606 CGCTTTTGTCTCACTGCGGCCAATACCTTCATGTTCCAAAGTCGGTGGATCCTT 547
QY 157 YAlaLysAlaValIleSerArgGlyGlu-TyrGlyValProAlaArgGlyAsnAsnCys 176
DB 546 ATGCTAAGCAGTGATATAAGCGGAGGAGTATGGTGTTCAGCGCGTGGTAACAATTGC 487
QY 177 TrpProGln-MetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAs 196
DB 486 TGGCCTCAAGATGGCTGGCATATATCCCTTTCATATAGCACGTTTGATTTGAAAGGCGA 427
QY 196 pLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPh 216
DB 426 CCTACCTCTAAGATATCTTCAAAGGACCTGGTATATATAGATGCACTTCGCTGGGAT 367
QY 216 eThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys 236
DB 366 CAGAAGCATGATTCAGCAATGTAGACATCCGGGTACTTTTCATTTGGAGCTGTGTCCGA 307
QY 236 sLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPh 256
DB 306 GCTTGACTATTTCAGGAGCTTGGAGTTAATTGTATTGAATTAATGCTCCATGAGTT 247
QY 256 eAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheThrTrpGlyTyrSerThrI 276
Db 246 CAACGAGCTGGAGTACTCAACCTCTTCTCCAGATGAACCTTTTGGGATATTTACCAT 187
QY 276 eAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAs 296
Db 186 AAACCTCTTTTACCAATGACAGATACATACAGCGGGGATAAAAAACTGTGGCGGTGA 127
QY 296 pAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValI 316
Db 126 TGCATAAATAGTTCAAAACTTTTGAAGAGAGGCTCACAACCGGGAATTTGAGGTGAT 67
QY 316 eLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPh 336
Db 66 CCTGAATGTTGCTTCCACCATACAGCTGAGGGAATGAGATGGTCCAGTATTGTCATT 7
QY 336 eLys 337
Db 6 TAAG 3
RESULT 2
BQ609582 737 bp mRNA linear EST 25-JUN-2002
LOCUS BR15559 wheat EST endosperm library Triticum aestivum cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BQ609582 GI:21558921
VERSION BQ609582.1
SOURCE Triticum aestivum (bread wheat)
KEYWORDS Triticum aestivum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 737)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
sequences
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
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            /db_xref="taxon:4565"
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            /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
            (days post anthesis)"
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Pred. No.: 7,25e-114 Length: 737
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Percent Similarity: 90.20% Conservative: 8
Best Local Similarity: 86.94% Mismatches: 18
Query Match: 26.52% Indels: 6
DB: 13 Gaps: 2
US-09-674-817B-3 (1-764) x BQ609582 (1-737)
QY 291 LysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLys 310
Db 3 AAAAATGTGGGGCTGATGTCATAAATGAGTTTCAAAACTTTTGTAAAGAGAGGCTCACA 62
QY 311 ArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsn 330

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Db      63  CCGGGAATTGAGCTGATCTGGATGTTGTTCTTCAACCATACAGCTCAGGGTAATGAGAT 122
Qy      331 GlyProIleLeuSerPheIysGlyValAspAsnThrTyrTyrMetLeuAlaProLys 350
Db      123  GGTCGAATATATCATTTAGGGGGGTCGATAATACATACATATATATGTTGCACCCAG 182
Qy      351 GlyGluPheTyrAsnTyrSerGlyCysGlyValAsnThrPheAsnCysAsnHisProValVal 370
Db      183  GGAGAGTTTATAAATATCTGGCTGTGGGAATACCTTCAACTGAATCATCTCTGTGGTT 242
Qy      371 ArgGlnPheIleValAspCysLeuArgTyrTyrValThrGluMetHisValAspGlyPhe 390
Db      243  CGTCAATTCATTGATGATGTTTAAAGATATCGGGTCATGGAATAATGATCTTGATGTTT 302
Qy      391 ArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspProValAsnVal 410
Db      303  CGTTTGAATCTGCATCCATATGACACAGAGTTCCAGTCTGTGGATCCAGTTAACGTG 362
Qy      411 TyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThrProPro 430
Db      363  TATGGAGCTCCCAATAGAGGTGACATGATCACACAGGGACACCTCTTGGTACTCCACCA 422
Qy      431 LeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIysLeuIleAlaGluAla 450
Db      423  CTTATTTGACATGATCAGCAATGACCCCAATCTTGGAGGGCTCAAGCTCATTTGCTGAAGCA 482
Qy      451 TrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPheProHisTyrPheAsnValTyrSerGlu 470
Db      483  TGGGATGACAGGAGGCTCTATCAAGTAGGTCAATTTCTCTCACTGGAAATGTTGGTCTGAG 542
Qy      471 TrpAsnGlyTyrTyrArgAspIleValArgGlnPheIleLysGlyThrAsp-GlyPheAl 490
Db      543  TGGAAATGGGAAGTACCGGACATTTGGCCCAATTTCTTAAAGGCACCTGGTGGGATTTGT 602
Qy      490 aGlyGlyPheAla--GlyCysLeuCysGlySerProHisLeuTyr--GlnAlaGlyGly 508
Db      603  TGGTGGTGTTCGCGAGCTCTTTGTGNAGTCCACACCTATTTCCCGGACGGGGAG 662
Qy      509 ArgLysPro-TrpHisSerIleAsn---PheValCysAlaHisAspGlyPheThrLeuAl 527
Db      663  GGGAAACCTTTGGCCCAATTTCAAAATTTGGTTGTGTCCTTGTGCTGATGATTTACACTGGG 722
Qy      527 aAspLeu 529
Db      723  GGGAAAT 729

CD897205      625 bp      mRNA      linear      EST 14-JUL-2003
G174.105C12F010823 G174 Triticum aestivum cDNA clone G174105C12,
mRNA sequence.
CD897205      1      GI:32671533
CD897205      1      (bases 1 to 625)
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 625)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003);
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers

FEATURES
RESULT 3
CD897205
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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/organism="Triticum aestivum"
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Alignment Scores:
Pred. No.: 3.45e-111 Length: 625
Score: 1092.00 Matches: 203
Percent Similarity: 99.02% Conservative: 0
Best Local Similarity: 99.02% Mismatches: 2
Query Match: 25.93% Indels: 2
DB: 14 Gaps: 0

US-09-674-817B-3 (1-764) x CD897205 (1-625)
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAla 563
Db 13 AACAGAGATGGAGAAAATCAATCTTAGCTGGAATTTGTGGGAGGAGGAATTCGCA 72
Qy 564 ArgLeuSerValIysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583
Db 73 AGATTGCTGTCAAAAGATTGAGAGAGGACAGATGCGCAATTTCTTTGTTGTCATG 132
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603
Db 133 GTTTCTCAAGAGTCCAAATGTTCTACATGGTGATGAATATGCCACACAAAAAGGGGC 192
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGlu 623
Db 193 AACACAATACATACCTCCCATGATTCITATGTCAATTTTTCGTGGGATAAAAAGAA 252
Qy 624 GlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArgLysGluCysGlu 643
Db 253 CAATACTCTGAGTTGCACCGATTCTGTGCTCATGACCAATTCGCAAGGAGTGCAG 312
Qy 644 GlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnPro 663
Db 313 GGTCTTGCCCTTGAGGACTTTCAGCGGCCAAACGGCTGCAGTGGCATGTCATCAGCT 372
Qy 664 GlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArg 683
Db 373 GGGAGGCTCATTTGGTCTGAGATAGCCGATTCTGTTGCCCTTTTCCATGAAGATGAAGA 432
Qy 684 GlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuPro 703
Db 433 CAGGGCGAGATCTATGTGGCTTCAACACGACCTTACCGGCCCTTGTGTGAGCTCCA 492
Qy 704 GluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAlaProTyrAsp 723
Db 493 GAGCGCGAGGGCGCGGTGGGAACCGGTGGTGGACACAGCGAAGCCAGCACCATTAGAC 552
Qy 724 PheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeu 743
Db 553 TTCTCTCACCAGCAGCTTACT-GATCGCGCTCTCACCATACACAGTTCCTCGCATTC-CTC 610
Qy 744 TyrSerAsnLeuTyr 748
Db 611 TATCCAACTCTTAC 625

RESULT 4
BU997255
LOCUS
DEFINITION
5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
EST.

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SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 617)
AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
TITLE EST sequencing and analysis in barley (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 617 Std Error: 0.00
Plate: 7 row: G column: 18
Seq primer: M13rev.

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/db_xref="taxon:112509"
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/dev_stage="female inflorescences (approx. 3 mm in size)"
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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN
Alignment Scores:
Pred. No.: 3,51e-109 Length: 617
Score: 1074.00 Matches: 192
Percent Similarity: 97.03% Conservative: 4
Best Local Similarity: 95.05% Mismatches: 6
Query Match: 25.50% Indels: 0
DB: 13 Gaps: 0

US-09-674-817B-3 (1-764) x BU997255 (1-617)

QY 107 LeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyLeu 126
DB 11 CTTGACCCCTGATGATCGGACGTGGGACGTGGCATGCTCTCTCGTGGCGAGCTG 70
QY 127 HisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyr 146
DB 71 CACGGCATGCTTTATGGGTACAGGTCGACGGCACCTTCGCTCCTCCTACCTGGCGGCATAC 130
QY 147 LeuAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGlu 166
DB 131 TTGATGTTTCCAAATGTTGGTGGATCTTATGCTAAGCAGTATAGCGGGAGGAG 190
QY 167 TyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeu 186
DB 191 TATGGTGTTCGGCGCATGTTAAACAATGTCGGCCTCAGATGCTGGCATGATCCCTCTT 250
QY 187 ProTyrSerThrPheAspTyrGlyAspLeuProLeuArgTyrProGlnLysAspLeu 206
DB 251 CCATATAGCAGCTTGTATGGGAGGCGACCTACCTCTAAGATATCTCAAGAGGACCTT 310
QY 207 ValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHis 226

Db 311 GTAATATATGAGTGCACCTTGGTGGATTCCAGAACGATGATTCAGCAATGTAGACAT 370
QY 227 ProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsn 246
Db 371 CCGGGTACTTTCATTTGGGGCTGTGCGAAGCTTGACTATTTGAAGAGCTTGGAGTTAAT 430
QY 247 CysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSer 266
Db 431 TGTATAGAAATTAATGCCCTGCCATGAGTTCAACGAGCTGGAGTATGCAACCTCTCTTCC 490
QY 267 LysMetAsnPheTyrGlyTyrSerThrIleAsnPheSerProMetThrArgTyrThr 286
Db 491 AAGATGAACCTTTTGGGGATATCTACCAATAAACTCTTTCACCAATGACGAGTACAGC 550
QY 287 SerGlyGlyIleLysAsnCysGlyAspAlaIleAsnGluPheLysThrPheValArg 306
Db 551 TCAGTGGGATATAAAACCTGTGGCGTGATGGCATAAACGAGTTCAAAACTTTTGTAGA 610
QY 307 GluAla 308
Db 611 GAGTCT 616

RESULT 5
CB035933
LOCUS
DEFINITION
CB035933 655 bp mRNA linear EST 15-JAN-2003
VWA015B02.119888 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera cDNA clone VWA015B02 5, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CB035933
CB035933.1 GI:27755178
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (Bases 1 to 655)
Cramer, G.R. and Cushman, J.C.
An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1318
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 015 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 655.
Location/Qualifiers
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/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

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/clone="VWA015B02"
/tissue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Alignment Scores:
Pred. No.: 7.74e-107 Length: 655

Score: 1053.50 Matches: 179
 Percent Similarity: 90.83% Conservative: 19
 Best Local Similarity: 82.11% Mismatches: 19
 Query Match: 25.01% Indels: 1
 DB: 14 Gaps: 1

US-09-674-817B-3 (1-764) x CB035933 (1-655)

QY 456 LeuTyrGlnValGlyGlnPheProHisTyrAsnValTyrSerGluTyrAsnGlyLysTyr 475
 Db 1 CTTTACCAAGTTGGCATGTTCTCTCACTGGGTCCTTGTGTCAGATGGATGGAGATAT 60
 QY 476 ArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGlu 495
 Db 61 CGTGACATAGTCGGCAGATTATTAAGGTTTCAGATGGATTTCTCGGGCTTTGCTGAA 120
 QY 496 CysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProThrHisSerIle 515
 Db 121 TGCCTTTGTTGGAGCCCTATCTGTACAGAGAGGAGGAGAAACCTTGGAAACAGTATC 180
 QY 516 AsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTyrTrpAsnLysLys 535
 Db 181 AACTTTGTGTGGCCACATGATGTTTTACGTTGGCTGATTTAGTGACATACACAAAGAG 240
 QY 536 TyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsn 555
 Db 241 CATACAAATGCAATGGAGGACACAAATGATGGGAGAAATCATATAACACAGCTGGAAC 300
 QY 556 CysGlyGluGlyGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMet 575
 Db 301 TGTGGCAAGAAGGAGAGTTTCAGATATTTTCAGTAAGAATAATGAGGAAACACAAATG 360
 QY 576 ArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAsp 595
 Db 361 CGAAATTTCTTTCTTGTGCTCATGTTTCCCAAGTGTCCCTATCATCATACATGGTGTAT 420
 QY 596 GluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsn 615
 Db 421 GAATATGTTTACACAAAGGGGGACACAAATAGATTTGCCATGATAACTATATGAAC 480
 QY 616 TyrPheArgTyrAspLysLysGluGln---TyrSerGluLeuHisArgPheCysCysLeu 634
 Db 481 TACTTCCGATGGGATAAAGAAAGAGTCAATATCTGATTTCTTCAGATTTTGTGCTT 540
 QY 635 MetThrLysPheArgLysGlyCysGluGlyLeuGlyLeuGluAspPheProThrAlaLys 654
 Db 541 ATGTCCAAATTCGGCAGAAATGCCAGTCACTTGGCTTAAATGACTTCCCAACACGACAG 600
 QY 655 ArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSer 672
 Db 601 AGGCTGCAGTGGCATGGGGCCACCCCTGGGATGCCAGACTGGTCTAAACACAGC 654

RESULT 6

BJ267405 590 bp mRNA linear EST 09-APR-2002
 LOCUS
 DEFINITION
 aestivum unpublished cDNA library, wh_oh Triticum
 accession
 version
 keywords
 source
 organism

BJ267405
 BJ267405
 BJ267405.1 GI:20087755
 EST

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

1 (bases 1 to 590)
 Ogihara, Y. and Murai, K.

Expressed genes in Triticum aestivum
 Unpublished (2002)

Contact: Tadasi Shin-i

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

RESULT 7

BJ444934

LOCUS

DEFINITION

arborum cDNA clone GA_Ea002623f, mRNA sequence.

accession

version

keywords

EST

EST

EST

EST

EST

EST

EST

Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tsunigenes.nig.ac.jp.
 Location/Qualifiers
 1. 590
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whoh1f13"
 /tissue type="pistil at heading date"
 /dev stage="Peekes" scale 10.5"
 /clone_lib="Y. Ogihara unpublished cDNA library, wh_oh"

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 9.5e-107 Length: 590
 Score: 1052.00 Matches: 187
 Percent Similarity: 96.94% Conservative: 3
 Best Local Similarity: 95.41% Mismatches: 6
 Query Match: 24.98% Indels: 0
 DB: 12 Gaps: 0

US-09-674-817B-3 (1-764) x BJ267405 (1-590)

QY 543 AsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysGlyGluGlyGluPhe 562
 Db 3 AACCAACAGNATGCGAATAATACAACTTAGCTGGATTTGTGGGAGGAGGAATTC 62
 QY 563 AlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeu 582
 Db 63 GCAAGATTGTCTGTCAAAGATTGAGGAGAGGAGATGCGCAATTTCTTTGTTGTC 122
 QY 583 MetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGly 602
 Db 123 ATGTTTCTCARGAGTTCCAAATGTTTATATGGCATGAGTATGCGCAACAAAAGG 182
 QY 603 GlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLysLys 622
 Db 183 GGCACCAACAAATACATACCTGCCATGATTTCTATGTCAATTTATTTTCCTGGATATAAAA 242
 QY 623 GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642
 Db 243 GACAAATACCTCTCACTTGCACCGATTTCTGTGCTCATGACCAATTTCCGCAAGAGTGC 302
 QY 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662
 Db 303 GAGGCTCTTGGCTTGAGGATTTCCACGCGCCGACGCTGAGTGGCATGTGTCATCAG 362
 QY 663 ProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
 Db 363 CCTGGGAAGCCTGATTTGCTGAGAATAGCCGATTCGTTGCCCTTTCCATGAAAGATGAA 422
 QY 683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
 Db 423 AGACAGGGCGAGATCTATGTGGCTTTCAACACGACCACTTACCGCCGCTTGTGTAGCTC 482
 QY 703 ProGluArgAlaGlyArgArgTyrGluProValValAspThrGlyLysProAlaProTyr 722
 Db 483 CCGAGCGCACAGGGCGCGGTGGGAACCGGTGGTGGACACAGGCAAGCCAGCCACCATAC 542
 QY 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGln 738
 Db 543 GACTTCTCACTGACGACTTACCTGATCGGCTCTCACCATACACCAG 590

RESULT 7

BJ444934

LOCUS

DEFINITION

arborum cDNA clone GA_Ea002623f, mRNA sequence.

accession

version

keywords

EST

EST

EST

EST

EST

EST

EST

SOURCE
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 913)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,
Henry, D., Wood, I.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCCTATAGGG
High quality sequence stop: 777.
Location/Qualifiers
i . 913
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="CA_Ea026823f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

FEATURES
source
1..913
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="CA_Ea026823f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 6,65e-105 Length: 913
Score: 1038.50 Matches: 202
Percent Similarity: 79.66% Conservative: 33
Best Local Similarity: 68.47% Mismatches: 51
Query Match: 24.66% Indels: 11
DB: 12 Gaps: 4
US-09-674-817b-3 (1-764) x BG444934 (1-913)

QY 162 IleserArgGlyGluTyrGlyValProAlaAaGGlyAsnAsnCysTrpProGlnMetAla 181
Db 26 ATAGCAGAGGGAGGTTGGGGCTTTAGGCGCTGAAGATAATTGTTGGCCCAATGGCC 85
QY 182 GlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyr 201
Db 86 GGAATGGTGCTACTTTCAGAAATATCATGATTTGATGGGAAGGTCATTACCTTTGAGACAT 145
QY 202 ProGlnIleAspLeuValIleTyrGluMetHisLeuArgGlyPheThrIleHisAspSer 221
Db 146 CCACAGAGATCTCAATATTTACGAATATCATGCGTGGATATACAAGATGAATCT 205
QY 222 SerAsnValGluHisProGlyThrPheIleGlyAlaValSerIleAspLeuAspTyrLeuIys 241
Db 206 AGTGGGCAAAATTTCTCGACAGTATCGTGTGTGGTGAAGGCTTGACCACTTAAG 265
QY 242 GluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyr 261
Db 266 GAACCTTGGAGTCAACTGCATGAATTAATGCCATGTCAGAAATTCATGAGTTGAGATC 325
QY 262 SerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSerThrIle 276
Db 326 TACAGCTACAATCTGTTTTGGGTGACTATAGTTGAATCTTTGGGCAATTCACAAATC 385
QY 277 AsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleIleAsnCysGlyArgAsp 296
Db 386 AATTATTTTCCCCCATGATGAAGGATATTCATCTTCTGGTATTCGTAGCTGTGCTGTAT 445

QY 297 AlaIleAsnGluPheIysThrPheValArgGluAlaHisLysArgGlyIleGluValIle 316
Db 446 GCATTTAATGAATTCATAATCTTTTAAAGAAGCACATAAACCGGGAATTCAGGTTATA 505
QY 317 LeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPhe 336
Db 506 ATGGATGTTGTTTCAATCACACAGCTGAAGGCGCATGAAAGGTCCTCAGTTTGTCAATT 565
QY 337 LysGlyValAsnAsnThrThrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyr 356
Db 566 AGAGGTGTTGATTAACGTCTCTATTACATGCTGGCACCTAAGGAGAGTACTACATTAAT 625
QY 357 SerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAsp 376
Db 626 TCAGGGTGTGGGAACACATTCACCTGTGACCATCTCTGTGTCGTCAATTTATATATAGAC 685
QY 377 CysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396
Db 686 TGCTTAAGATATTGGGTAAACAGAAATGCAATGTCGATGGGTGCGTTGATCTTGTCTTCC 745
QY 397 IleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGlu 416
Db 746 AT-ATGACCAGAGTAGCGGTCTTTGGGATCA-GTAAATGTTATGGCA---GATCTTGAG 800
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProLeuIleAspMetIleSer 436
Db 801 AAGGGATTGGATCAACATGGC---CCCTCTCAACATCTCCATCGTTGGCTGAGTAGT 857
QY 437 AsnAspProIleLeuGlyValLysLeuIleAlaGluAlaTrp 451
Db 858 AAG-----ATCTGTACTCGGAGAGGAGCTATATCTGAGCATGG 896

RESULT 8
BQ865760 753 bp mRNA linear EST 14-AUG-2002
LOCUS OGC5M22.yg.ab1 OQ ABCDI lettuce salinas Lactuca sativa cDNA clone
DEFINITION OGC5M22, mRNA sequence.
ACCESSION BQ865760.1 GI:2251225
VERSION BQ865760.1 GI:2251225
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 753)
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compsgenomics.ucdavis.edu/
Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
COMMENT Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
Singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: OGC5 row: M column: 22.
Location/Qualifiers
1..753
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clones="OGC5M22"
/lab_host="E.coli"
/clone_lib="OQ ABCDI lettuce salinas"
/note="Vector: pBRCNAsfIAB; The library was constructed

from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/> TAG_SEQ=Not found"

ORIGIN

Alignment Scores:
 Pred. No.: 1,45e-100 Length: 753
 Score: 998.50 Matches: 182
 Percent Similarity: 80.93% Conservative: 26
 Best Local Similarity: 70.82% Mismatches: 32
 Query Match: 23.71% Indels: 17
 DB: 13 Gaps: 2

US-09-674-817B-3 (1-764) x BQ865760 (1-753)

QY 177 TrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAsp 196
 Db 10 TGGCCG-----CTTGACGGGAAGAGAT 33

QY 197 LeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPhe 216
 Db 34 CTGCCCTGTCAATTCACAAAGAGATCTGGTGATTTATGAATGATGATTCGTGGATT 93

QY 217 ThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys 236
 Db 94 ACAAGCATGAGTCCAGTAAGACAGAGTCTCTGGTACTTACTTGGTGTAGTGGAATA 153

QY 237 LeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPhe 256
 Db 154 CTGTATCATTTAAAGAACTTGTTGTAACCTCATAGATTTAATGCCATGCCATGATTC 213

QY 257 AsnGluLeuGluTyrSerThr-----SerSerSerLysMetAsnPheTrp 271
 Db 214 ATAGCTGGAGTACTTACGATACATCTGCTGGGTGACTACAGGTAAATTTATGG 273

QY 272 GlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyIleLys 291
 Db 274 GGGTATTCAACTATCAATTAATCTTCCACCTATGTTGAGATATGATCTCTGCTGGTGGT 333

QY 292 AsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArg 311
 Db 334 ATGTGGCCTTGATGCAATAAATAGTTCAAAACAACTTTATTAAGAGGCACACAAACGT 393

QY 312 GlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGly 331
 Db 394 GGAATCGAGGTCTCATGATGTTGTTTCAATCACACCTGCTGAAGGGAATGAAATGGT 453

QY 332 ProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGly 351
 Db 454 CCCATTGCTCTTTGAGGTGTTGATACAGTGTCTTTTATATCTTTCACCTAAAGGA 513

QY 352 GluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArg 371
 Db 514 GAGTCTCAACTATTCAGATGTGGAACACACATTCACCTGCAACCATCTTATGTGGCC 573

QY 372 GlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArg 391
 Db 574 CAATTTATAGTAGATTCCTTTGAGATATTGGGTAAACAGAGATGCATGTAGATTCGA 633

QY 392 PheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyr 411
 Db 634 TTGTATCTTGCTCTATCATGACAGAGCCAGCATCTTTTGTATGCGATTAATGATAT 693

QY 412 GlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428
 Db 694 CGAATCAAGTAGAAGATGATTACTGACACCGGGTCTATCTCTCATCACC 744

RESULT 9

BE493792

LOCUS

DEFINITION

WHE1275_E05_I092S Secale cereale

cDNA clone WHE1275_E05_I09, mRNA sequence.

ACCESSION

BE493792

VERSION

BE493792.1

KEYWORDS

EST.

SOURCE

Secale cereale (rye)

ORGANISM

Secale cereale

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Secale.

1 (bases 1 to 578)

Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat genomes - Another cDNA library from rye

Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 510595773

Fax: 510595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..578

/organism="Secale cereale"

/mol_type="mRNA"

/cultivar="Blanco"

/db_xref="taxon:4550"

/clone="WHE1275_E05_I09"

/tissue_type="Anther"

/dev_stage="Adult plant before anthesis"

/lab_host="E. coli SOLR"

/clone_lib="Secale cereale anther cDNA library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Alignment Scores:

Pred. No.: 2,29e-99 Length: 578

Score: 986.00 Matches: 179

Percent Similarity: 96.34% Conservative: 5

Best Local Similarity: 93.72% Mismatches: 7

Query Match: 23.41% Indels: 1

DB: 10 Gaps: 0

US-09-674-817B-3 (1-764) x BE493792 (1-578)

QY 543 AsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlyGluPhe 562

Db 6 GACAACAGAGATGAGAAAATAC-AATCTTAGCTGGAATCTGGGAGGAGAGATTC 64

QY 563 AlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheValCysLeu 582

Db 65 GCAGATGTCAGTCACAAAGATGAGAGAGGAGAGATGCGCAATTCCTTGTTCCTC 124

QY 583 MetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGly 602
 Db 125 ATGGTTTCTCAAGAGATTCCAAATGTTTACATGGCGCATGAATATGGCCACACAAAGGG 184
 QY 603 GlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLys 622
 Db 185 GGCACACAAATACATACATGCTATGATCTTAATGTCATTAATTTTCGCTGGATTAATAA 244
 QY 623 GluGlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArgLysGluCys 642
 Db 245 GAACAATACCTGACTGTGACGATTCTGCTGCTCATGACCAAAATTCGCAAGAGTGC 304
 QY 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTyrHisGlyHisGln 662
 Db 305 GAGGGTCTTGGGCTTGGAGACTTTCCAAACGGCTGAACGGTTCAGTGGCATGGTTCATCAG 364
 QY 663 ProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
 Db 365 CTGGGAAGCTTGATGGTCTGAGAAAGCCGATTCGTTGCTTTTCCATGAAGATGAA 424
 QY 683 ArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
 Db 425 ACAAAAGAGTGCAGATCTATGCGCTTCAACACCGCCACTTACCGGCGGTTGTTGAATC 484
 QY 703 ProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysProAlaProTyr 722
 Db 485 CCAGAGCGCACAGGCGACCGCTGGGACCGCTGGTGGACACAGGAAGGACCATAT 544
 QY 723 AspPheLeuThrAspAspLeuProAspArgAla 733
 Db 545 GACTTCTCACCACGACTTACCTGATCGCGT 577

RESULT 10

CA781552 637 bp mRNA linear EST 03-DEC-2002
 LOCUS 024A03AF Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
 DEFINITION sequence.

ACCESSION CA781552

VERSION CA781552.1 GI:26019585

KEYWORDS Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 637)
 Lundgaard,M., Emmeren,J., Nielsen,K.L., Wilson,I., Somerville,S.
 and Wellinder,K.G.
 EST sequencing of Erysiphe cichoracearum infected Arabidopsis
 plants

TITLE

Unpublished (2002)

JOURNAL

COMMENT

Contact: Karen G. Wellinder
 Institut for bioteknologi
 Aalborg Universitet
 Sohngaardsklostervej 49, 9000 Aalborg, Denmark
 Tel: +45 96358467
 Fax: +45 98141808
 Email: kgw@bio.au.dk.

FEATURES

source

1 637
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /dev_stage="Plant 3 weeks old, three days post infection"
 /clone_lib="Infected Arabidopsis Leaf"
 /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
 library of Arabidopsis and E. cichoracearum infected leaf
 from three weeks old Arabidopsis plants. Plants were
 harvested 3 days after infection and mRNA oligo dt
 selected."

ORIGIN

Alignment Scores:
 Pred. No.: 9,88e-99 Length: 637
 Score: 981.00 Matches: 172
 Percent Similarity: 89.05% Conservative: 15
 Best Local Similarity: 81.90% Mismatches: 20
 Query Match: 23.29% Indels: 3
 DB: 14 Gaps: 2

US-09-674-817B-3 (1-764) x CA781552 (1-637)

QY 445 LysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPheProHis 464
 Db 12 AACCTAATAGCTGAACATGGATGGCGTGGCTGTACCAAGTGGCATGTTTCCACAC 71
 QY 465 TrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheLys 484
 Db 72 TGGGGTATTTGGTCTCAGTGGAAATGGAAGTTTCGGGATGTTGTGAGACAGTTTCAATAA 131
 QY 485 GlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyr 504
 Db 132 GGACCGATGGCTTTTCTGGTGTCTTTTGTGAATGCTCTGTGGAAGCCAAATCTGTAC 191
 QY 505 GluAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisaspGlyPhe 524
 Db 192 CAG---GGAGGTAGGAACCTTGGCACAGCATCAATTTTATATGTGCGCATGATGTTTT 248
 QY 525 ThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsn 544
 Db 249 ACCTTGGCAGATTAGTACTTACACAAATAGATAAATCTGGCAATGGAGAGAGAT 308
 QY 545 ArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGluPheAlaArg 564
 Db 309 AATGATGGAGAGAATCACAAATTACAGCTGGAACCTGTGGAGAGGAGGAGACTTTGCGAGT 368
 QY 565 LeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetVal 584
 Db 369 ATCTCGGTGAAGAGACTAAGGAACACAGATCGGAAATTTCTTTGTTTCCCTCATGGTT 428
 QY 585 SerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyLysAsn 604
 Db 429 TCCCAAGGTGTCCCAATGATTTACATGGGAGATGAATATGGCCATATAAAGGGGAAAC 488
 QY 605 AsnAsnThrTyrCysHisaspSerTyrValAsnTyrPheArgTrpAspLysGluGln 624
 Db 489 AACACACGTATTGCCATGACAACTATATGAACATTTTCGGTGGGATACAAAGGAAGA 548
 QY 625 ---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys-GI 643
 Db 549 GCACATTCGACTTCTCAGATTCTGCGGTATTTCTTATCAAGTTTCGTGATGAATCTTGA 608
 QY 643 uGlyLeuGlyLeuGluAspPheProThr 652
 Db 609 ATCATTGGCTTGAATGATTCCCAACA 636

RESULT 11

CA199345 697 bp mRNA linear EST 25-SEP-2003
 LOCUS SCRLFL1011G11.9 FL1 Saccharum officinarum cDNA clone SCRLFL1011G11
 DEFINITION 5', mRNA sequence.

ACCESSION CA199345

VERSION CA199345.1 GI:35231514

KEYWORDS EST

SOURCE

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 697)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

AUTHORS

TITLE

The libraries that made SUCEST

JOURNAL

COMMENT

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parrada@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccc.br/center.fcav.unesp.br

Plate: 011 row: G column: 11
Seq primer: T7 Promoter Primer.

FEATURES

Location/Qualifiers
1..697

source

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCLFL1011G11"

/lab_host="DH10B"

/clone_lib="FL1"

/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [inflorescence at beginning of development (1cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucet.lad.ic.unicamp.br/public"

ORIGIN

Alignment Scores:

Pred. No.: 6.19e-98 Length: 697
Score: 974.50 Matches: 179
Percent Similarity: 91.79% Conservative: 11
Best Local Similarity: 86.47% Mismatches: 16
Query Match: 23.14% Indels: 1
DB: 14 Gaps: 1

US-09-674-817B-3 (1-764) x CA199345 (1-697)

QY 559 GluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGluMetArgAsnPhe 578
Db 1 GAAGGAGATTTCGAGTTTGTTCAGTCCGAAATTAAGGAAGAGCAATTCGCAATTTT 60
QY 579 PheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGly 598
Db 61 TTTGTTTGTCTGATGTTTCTCAGGAGTTCGAAATGTTCTACATGGCGATGATATGTT 120
QY 599 HisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArg 618
Db 121 CACACAAAGGAGGAGAAACAAATACATCTCCATGCCATGACCAATATGTCATTTTCGTT 180
QY 619 TrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLys 637
Db 181 TGGGATAAGAGGAAGAAACAATCTCTGATTGTGTACAGATTCTGCGCTCATGACCAA 240
QY 638 PheArgLysGlyCysGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGln 657
Db 241 TCCCGCAGGAATGTAATCTCTTGGTCTGTGAGGACTTCCGACTTCAGAACGGTTGCAA 300
QY 658 TrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPhe 677
Db 301 TGGCAGGTCATCAGCCTGGGAGGCTGACTGCTGGAGGAGCGGATTCGTTGCCCTTC 360
QY 678 SerMetLysAspGluArgGlnGlyLeuTyrValAlaPheAsnThrSerHisLeuPro 697
Db 361 ACCATGAGGATGAAACCAAGCGAGATCTACGTGGCTTCAACACCAAGCCACCTGCC 420
QY 698 AlaValValGluLeuProGluArgAlaGlyArgTgTgTgProValValAsnThrGly 717
Db 421 GTGGTCGTCGGCTTCCAGAGCGCCCTGTTTCCGATGGAGCCAGTGGTGGACACAGGC 480

QY 718 LysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHis 737
Db 481 AAAGAAGCACCTATGACTTCCTCACCAGCGTTTACACAGCCGTGCTGCACCGTTTAC 540
QY 738 GlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIle 757
Db 541 CAGTTCCTTCATTTCTCAACTCCAACTCTACCCCTATGCTTAGCTACTCTCTTATATC 600
QY 758 LeuValLeuArgProAspVal 764
Db 601 CCTGTATTGCGCCCTGATTT 621

RESULT 12

BU039907

LOCUS

DEFINITION

PP_LEA0004E05f Peach developing fruit mesocarp Prunus persica cDNA

clone PP_LEA0004E05f, mRNA sequence.

BU039907

VERSION

KEYWORDS

SOURCE

ORGANISM

Prunus persica (peach)

Prunus persica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 661)

Callahan,A., Palmer,M., Main,D., Wing,R. and Abbott,A.

Peach Model Genome for Rosaceae

Unpublished (2002)

Contact: Abbott, A.

Dept of Genetics and Biochemistry

Clemson University

122 Long Hall, Clemson University, Clemson, SC 29634, USA

Tel: 864 656 3060

Fax: 864 656 6879

Email: aalbert@clemson.edu

Total High Quality bases = 537

Seq primer: TAATACGACTCACTATAGG

High quality sequence stop: 661.

Location/Qualifiers

1..661

/organism="Prunus persica"

/mol_type="mRNA"

/cultivar="Loring"

/db_xref="taxon:3760"

/clone="PP_LEA0004E05f"

/tissue_type="Mesocarp"

/lab_host="E. coli"

/clone_lib="Peach developing fruit mesocarp"

/note="Vector: pBluescript II SK(-); Site_1: EcoRI;

Site_2: XhoI; authority=Prunus persica L. Batsh; The

sequence has been trimmed to remove vector sequence and

contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis go to

http://www.genome.clemson.edu/projects/peach. To order

this clone go to http://www.genome.clemson.edu/orders"

ORIGIN

Alignment Scores:

Pred. No.: 4.64e-95 Length: 661
Score: 948.50 Matches: 163
Percent Similarity: 87.16% Conservative: 27
Best Local Similarity: 74.77% Mismatches: 27
Query Match: 22.52% Indels: 1
DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x BU039907 (1-661)

QY 542 GluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlyGlu 561
Db 3 GAACACAAATGATGAGAGAGTCTAATAATAGCTGGAATGTGACAGAGGAGAGAG 62

	QY	562	PheAlaArgLeuSerValLysArgGluUArgGlyArgGlnMetArgAsnPhePheValCys	581
	Dd	63	TTCGCAGCGCATTTTCTAGTGAAAGAATTCGAGAAAACGCAAAATGGGAATTTTTTTGTGTGC	122
	QY	582	LeuMetValSerGInGlyWalProMetPheTyrMetGlyAaspGluTyrGlyHisThrIlys	601
	Dd	123	CTCATGGTTTCCCAAGGTTGCCAATGATAATATTGGTGATGAATATGGTCATCACAAA	182
	QY	602	GlyGlyAsnAsnAsnThrTyrCysHisAaspSertYrValAsnTyrPheArgrTrpAspLys	621
	Dd	183	GGAGAAACAACACACATATTGCCATGATAATTATTAATTACTTTTCGTGGGATAAG	242
	QY	622	LysGluGlnTyrSer---GluLeuHiIArpPheCysCysLeuMetThrlzIyIsPheArgIyls	640
	Dd	243	AAGGAAGAGTCTCTATTGGACTTTTTCAGACTTTTTCGTGCTTATGACC AAAATTCGGCCC	302
	QY	641	GluCysGluGlyLeuGlyLeuGlubspPheProThrAlalysArgLeuGlnTrpHisGlyl	660
	Dd	303	GAATCCGAGTCAC TGGGCTTAATAATGACTTCCCAACAGACAGAGGCTGCAGTGCGCATGT	362
	QY	661	HisGlnProGlyLyIsProAspTrpSerGluAsnSerArgPheValAlaPheSerMetIyls	680
	Dd	363	CATGCTCTCGGGTACCAGACTGTGCTGMAAACAGCGCTTTCTGTGCTTTACTCTGATG	422
	QY	681	AspGluA-rgGInGlyGluILEtyrValAlaPheAsnThrsHisIeUpProLaValVal	700
	Dd	423	GACTCAGTGAAGAGAGAGCTGTATATTGCTTTCAATGCCAGCCATTTACCGCAACCAT	482
	QY	701	GluLeuProGluUArgAlaGlyArgArGrTrpCluproValValAspThrGlyIylsProAla	720
	Dd	483	ACACTGCCAGAGAGCCCTGGATACAGATGGGATCCCTTGGTAGACAC CAGAACGCTGCT	542
	QY	721	ProTyrAspPheLeuThrAspAspLeuProAspArgAlatHeurHleHisGlnPheser	740
	Dd	543	CCAATTGACTTTCTCTTCTAGTGACTCTCCAGGAAGAGATATTGCAAGTTAAACAGTACGT	602
	QY	741	HisPheLeuTy-SerAsnLeuTy-ProMetLeuSerTyrSerSerVallIeU	758
	Dd	603	CACTTCTTGAGCAAATTTATATCTCATGCTAGTATCTTCAATCATCTCAATCATCTCA	656

RESULT 13	CF041929	LOCUS	CF041929	622 bp	mRNA	linear	EST 17-JUL-2003
CF041929			OCI31h03	vs	OCI	Zea mays	OCI31h03, mRNA sequence.
DEFINITION							

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CF041929.1	GI:32937110	BST.	Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea
CF041929.1	GI:32937110	BST.	Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea

REFERENCE	1 (bases 1 to 622)
AUTHORS	Genoplate.
TITLE	Genoplate, a major partnership french program in plant genomics
JOURNAL	Unpublished (2003)
COMMENT	Contact: Genoplate

ORIGIN

Alignment Scores:
 Pred. No.: 1,51e-94 Length: 622
 Score: 943.50 Matches: 171
 Percent Similarity: 93.40% Conservatives: 13
 Best Local Similarity: 86.80% Mismatches: 12
 Query Match: 22.40% Indels: 1
 DB: 14 Gaps: 1

US-09-674-817B-3 (1-764) x CF041929 (1-622)

Qy	569	ArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVal	588
Dd	4	CGSGTAAAGGAGGCAATGCGCAATTCCTTTGTTGTTCTCAGGAGATT	63
Qy	589	ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyr	608
Dd	64	CCAATGTTCTACATGGCGCATGAATATGTCACAAAGGAGGAGCAACAATATCGTAC	123
Qy	609	CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLys--GluGlnTyrSerGlu	627
Dd	124	TGCATGACCAATTATGTCAACTATTCGTTGGGATAGAGGAAGAACAACTCTCTGAT	183
Qy	628	LeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeu	647
Dd	184	TTGTACAGATTTCGCGTCTCATGACCAATTCGCAAGAAATGTGAATCTCTTGGCCTT	243
Qy	648	GluAspPheProThrAlaLysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAsp	667
Dd	244	GAGGACTTCCGACTTCAGAACCGTTGAATGGCAGCGTCATCAGCCGGAAGCCCTGAC	303
Qy	668	TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIle	687
Dd	304	TGFTCAGAGCAAGCCGATTCGTTGCCTTCACCATGAAGGACGAAACCAAGCGAGATC	363
Qy	688	TyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly	707
Dd	364	TACGTGGCCTTCAACACCACTCCGCTGGTGTTCGGGGTTCAGAGCGCTCTGGG	423
Qy	708	ArgArgTrpGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAsp	727
Dd	424	TTCCGATGGAGCGCGTGTGGACACCGGCAAGAGGCACCATATGACTTCCTCCCGAT	483
Qy	728	AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu	747
Dd	484	GGCTACCAGATCGTGTGTGCACCGTCTACAGTCTCTCTCTCTCTCTCTCTCTCTCT	543
Qy	748	TyrProMetLeuSerTyrSerSerValIleLeuValLeuArgProAspVal	764
Dd	544	TATCCTATGCTAGCTACTCTCTCATCATCTCTGTTATTCGCCCTGATGTC	594
LOCUS	BU971724	536 bp	mRNA linear EST 22-OCT-2002
DEFINITION	HB19H1sr BC Hordeum vulgare subsp. vulgare cDNA clone HB19H15		
ACCESSION	BU971724		
VERSION	BU971724.1		
KEYWORDS	EST.		
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Hordeum vulgare subsp. vulgare		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.		
AUTHORS	1 (bases 1 to 536)		
TITLE	Rachuk.V., Zhang.H., Weschke,W., Fotokina,E. and Wobus,J.		
JOURNAL	Barley ESTs from developing seeds		
COMMENT	Unpublished (2002)		
	Contact: Stein Nils		
	Molecular Markers Group, Department Genbank		
	Institute of Plant Genetics and Crop Plant Research (IPK)		
	Corrensstr. 3, 06466, Gatersleben, Germany		

```

Tel: 039482-5522
Fax: 039482-5595
Email: stein@pk-gatersleben.de
Insert Length: 536 Std Error: 0.00
Plate: 19 row: H column: 15
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            /lab_host="XL10-Gold"
            /clone_lib="BC"
            /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."
ORIGIN
Alignment Scores:
Pred. No.: 1.33e-94 Length: 536
Score: 943.00 Matches: 169
Percent Similarity: 97.71% Conservative: 2
Best Local Similarity: 96.57% Mismatches: 4
Query Match: 22.39% Indels: 0
DB: 13 Gaps: 0
US-09-674-817B-3 (1-764) x BU971724 (1-536)

QY 135 PheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValVal 154
DB 12 TTCGAGCGGACCTTCGCTCTCTACTCGGGGCACTACTTGATGTTTCCAAATGTTGGTG 71
QY 155 AspProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsn 174
DB 72 GATCCTTATGCTAAGCCAGCTGATAGCCGGGAGGAGTAGTGTGTTCCGGCGCATGGTAAC 131
QY 175 AsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGlu 194
DB 132 AATTGCTGGCCCTCAGATGCTGGCATGATCCCTCTTCCATATAGCACGTTTGAATGGGAA 191
QY 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214
DB 192 GCGGACCTACCTTAAGATATCTCAAGAGGACCTGTATATATAGATGCACCTTGGT 251
QY 215 GlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVal 234
DB 252 GGATTCAACAGCATGATTCAAGCAATGTAGAACAATCCGGGTACTTTTCATTGGGGCTGTG 311
QY 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254
DB 312 TCGAGCTTGACTATTGAGGAGCTTGGAGTTAATTGTATAGAAATTAATGCCCTGCCAT 371
QY 255 GluPheAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSer 274
DB 372 GAGTTCAACAGCTGGGATGATGCAACCTCTCTTCCAAAGATGAACCTTTTGGGATATTCT 431
QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294
DB 432 ACCATAAATCTTTTTCACATGACGAGATACATGTCAGGTGGGATAAAAAATGTGGG 491
QY 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHis 309

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Db 492 CGTGATGCGATAAACGAGTTCAAAACCTTTTGTAAAGAGAGTCTCAC 536
RESULT 15
LOCUS BU970613
DEFINITION BU970613 BC Hordeum vulgare subsp. vulgare cDNA clone HB15C17
5-PRIME, mRNA sequence.
ACCESSION BU970613
VERSION BU970613.1 GI:24221406
KEYWORDS EST.
SOURCE
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        Hordeum vulgare subsp. vulgare
        Hordeum vulgare subsp. vulgare
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        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
        Pooidae; Triticeae; Hordeum.
        1 (bases 1 to 519)
        Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.
        Barley ESTs from developing seeds
        Unpublished (2002)
        Contact: Stein Nils
        Molecular Markers Group, Department Genbank
        Institute of Plant Genetics and Crop Plant Research (IPK)
        Corrensstr. 3, 06466, Gatersleben, Germany
        Tel: 039482-5522
        Fax: 039482-5595
        Email: stein@pk-gatersleben.de
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ORIGIN
Alignment Scores:
Pred. No.: 2.95e-90 Length: 519
Score: 904.00 Matches: 163
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Best Local Similarity: 96.45% Mismatches: 2
Query Match: 21.46% Indels: 0
DB: 13 Gaps: 0
US-09-674-817B-3 (1-764) x BU970613 (1-519)

QY 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254
DB 12 TCGAGCTTGACTATTGAGGAGCTTGGAGTTAATTGTATAGAAATTAATGCCCTGCCAT 71
QY 255 GluPheAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSer 274
DB 72 GAGTTCAACAGCTGGGATGATGCAACCTCTTCTTCCAAGATGAACCTTTGGGATATTCT 131
QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294

```

132	ACCA ¹ AAACT ¹ TCT ¹ TTT ¹ CACCAAT ¹ GACGAGAT ¹ TACAGT ¹ CAGT ¹ GGGAT ¹ AAAAA ¹ CTGTGG ¹	191
295	ArgAspAla ¹ IleAsnGluPhe ¹ LeuThr ¹ Phe ¹ Val ¹ ArgGlu ¹ Ala ¹ His ¹ Lys ¹ Arg ¹ Gly ¹ Ile ¹ Glu ¹	314
192	CGTGATGCATAA ¹ ACGAGT ¹ CAAA ¹ AACT ¹ TTT ¹ GTAAGAGAGT ¹ CTCACA ¹ ACCGGGAAT ¹ TGAG ¹	251
335	Val ¹ IleLeuAspVal ¹ Val ¹ Phe ¹ Asn ¹ His ¹ Thr ¹ Ala ¹ Glu ¹ AsnGlu ¹ AsnGly ¹ Pro ¹ Ile ¹ Leu ¹	334
252	GTGAT ¹ CTCGGAAT ¹ TGTCT ¹ CAACCATACACGTGAGGGT ¹ AATGAGAA ¹ TGGTCCGATATTA ¹	311
335	SerPhe ¹ Lys ¹ Gly ¹ Val ¹ AspAsn ¹ Thr ¹ Thr ¹ Tyr ¹ Met ¹ Leu ¹ Ala ¹ Pro ¹ Lys ¹ Gly ¹ Glu ¹ Phe ¹ Tyr ¹	354
312	TCATTTAGGGGGT ¹ GATAAT ¹ ACTACATACTATATGCTTGCACCCAAAGGGAGAGTTTAT ¹	371
355	Iasn ¹ Tyr ¹ Ser ¹ Gly ¹ Cys ¹ Gly ¹ Asn ¹ Thr ¹ Phe ¹ Asn ¹ Cys ¹ Asn ¹ His ¹ Pro ¹ Val ¹ Val ¹ Arg ¹ Gln ¹ Phe ¹ Ile ¹	374
372	AACTATTCTGCTGTGGGAAT ¹ ACCTTCAACTGTAAATCATCTCTGTGGT ¹ CGTCAATTTAT ¹	431
375	ValAsp ¹ Cys ¹ Leu ¹ Arg ¹ Tyr ¹ Trp ¹ Val ¹ Thr ¹ Glu ¹ Met ¹ His ¹ Val ¹ Asp ¹ Gly ¹ Phe ¹ Arg ¹ Phe ¹ Asp ¹ Leu ¹	394
432	GTAGATT ¹ GTGTTAAGNACTGGGTGATGGAAATGCATATTGATGGT ¹ TTT ¹ CGTTTGTGATCT ¹	491
395	AlaSer ¹ IleMet ¹ ThrArgGlySer ¹ Ser ¹	403
492	GCATCCATAAATGACCAGAGGTTCCAGT ¹	518

Search completed: August 10, 2004, 05:01:22
Job time : 4822 secs